

92655

STIC-Biotech/ChemLib

From: Mehta, Ashwin
Sent: Monday, April 28, 2003 4:11 PM
To: STIC-Biotech/ChemLib
Subject: sequence search

STIC,

Please search the commercial and interference databases for the following from 09/845,849:

- 1) the nucleotide sequence of SEQ ID NO: 1
- 2) the nucleotide sequence of SEQ ID NO: 3

My mail room is 9E12, office 9E07, art unit 1638.

Thank you,
Ashwin

Ashwin Mehta
United States Patent and Trademark Office
Biotechnology Patent Examiner
703-306-4540

Point of Contact:
Toby Port
Technical Info. Specialist
CM1 6A04
703-308-3534

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 4/29
Date Completed: 5/5
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 15:58:02 ; Search time 2798 Seconds

(without alignments)
8903.503 Million cell updates/sec

Title: US-09-845-849-1

Sequence: 1 tctgaactagatgacccccc.....aaaaaaaaaaaactcgag 856

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

```
GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pin:*
35: em_htg_rnd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	856	100.0	856	6	ARI48907	ARI48907 Sequence
2	842.4	98.4	855	6	ARI48906	ARI48906 Sequence
3	799.6	93.4	864	8	AB027504	AB027504 Arabidops
4	763.4	89.2	840	8	AY065378	AY065378 Arabidops
5	635.6	74.3	780	8	AB027505	AB027505 Arabidops
6	559	65.3	559	8	AY133813	AY133813 Arabidops
7	528	61.7	528	6	E38985	E38985 Method for
8	466	54.4	109560	8	F5114	AC001229 Sequence
9	465	54.3	2483	8	AF152096	AF152096 Arabidops
10	389.8	45.5	799	8	AB027506	AB027506 Arabidops
11	377.6	44.1	528	8	AF152907	AF152907 Arabidops
12	374.4	43.7	528	6	E38986	E38986 Method for
13	289.6	33.8	745	8	AB027456	AB027456 Citrus un
14	248.8	29.1	899	6	AX478001	AX478001 Sequence
15	248.4	29.0	847	8	AB052943	AB052943 Oryza sat
16	248	29.0	847	8	AB052944	AB052944 Oryza sat
17	239.8	28.0	1004	6	AX478049	AX478049 Sequence
18	238.6	27.9	866	8	AB062676	AB062676 Oryza sat
19	230.4	26.9	1191	6	AX478007	AX478007 Sequence
20	225.2	26.3	1078	6	AX477997	AX477997 Sequence
21	220.6	25.8	886	6	AX478033	AX478033 Sequence
22	196	22.9	836	6	AX478029	AX478029 Sequence
23	187	21.8	969	6	AX478027	AX478027 Sequence
24	185.8	21.7	492	6	AX477991	AX477991 Sequence
25	176.8	20.7	668	6	A61530	A61530 Sequence 4
26	176.8	20.7	668	8	ATU07674	U7674 Arabidops
27	175	20.4	837	6	AX478005	AX478005 Sequence
28	174.4	20.4	954	8	AF316419	AF316419 Lolium pe
29	171.6	20.0	950	8	AF159882	AF159882 Oryza sat
30	168.8	19.7	597	8	AB024715	AB024715 Arabidops
31	168.4	19.7	886	8	AY065211	AY065211 Arabidops
32	168.4	19.7	613	6	AX478043	AX478043 Sequence
33	166.8	19.5	559	8	AY096515	AY096515 Arabidops
34	166.4	19.4	980	6	AX478011	AX478011 Sequence
C 35	164	19.2	109936	8	ATPEF13	AL080253 Arabidops
36	164	19.2	197568	8	ATCHRIV53	AL16553 Arabidops
37	160.6	18.8	577	8	AF145259	AF145259 Nicotiana
38	159.4	18.6	902	6	AX478009	AX478009 Sequence
39	159	18.6	907	8	AF159883	AF159883 Oryza sat
40	157.6	18.4	1295	6	AX478021	AX478021 Sequence
41	154.8	18.1	560	8	AF145260	AF145260 Nicotiana
42	154.4	18.0	869	8	LEU84140	U84140 Lycopersico
43	146.8	17.1	558	8	AF145261	AF145261 Nicotiana
C 44	145.8	17.0	4377	8	ATU07834	U07834 Arabidops
45	136	15.9	354	8	AF145262	AF145262 Nicotiana

ALIGNMENTS

RESULT 1
ARI48907/c
LOCUS ARI48907 856 bp DNA
DEFINITION Sequence 3 from patent US 6225530.
ACCESSION ARI48907
VERSION ARI48907.1 GI:15112997
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 856)
AUTHORS Weigel, D. and Kaul, I.
TITLE Flowering locus T (FT) and genetically modified plants having
modulated flower development
JOURNAL Patent: US 6225530-A 3 01-MAY-2001

FEATURES Location/Qualifiers
Source 1..856 /organism="unknown"
BASE COUNT 249 a 194 c 150 g 263 t
ORIGIN

Query Match 100.0%; Score 856; DB 6; Length 856;
Best Local Similarity 100.0%; Pred. No. 7.1e-192;
Matches 856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTAGACTAGTGTATCCCGGGCTGCGAGAAATCAGACAGAGTTGTTCAAGATCAA 60
DB 856 TCTAGAACTAGTGTATCCCGGGCTGCGAGAAATCAGACAGAGTTGTTCAAGATCAA 797
QY 61 AGATGCTATTAATTAAGAGACCCTTATAGTAAGCAGAGTTGTTGAGACGTTCTTG 120
DB 796 AGATGCTATTAATTAAGAGACCCTTATAGTAAGCAGAGTTGTTGAGACGTTCTTG 737
QY 121 ATCCGTTTAATAGATCAATCACTCTAAAGGTTACTTATGCGCAAGAGAGTGAATAG 180
DB 736 ATCCGTTTAATAGATCAATCACTCTAAAGGTTACTTATGCGCAAGAGAGTGAATAG 677
QY 181 GCTTGATCTAAGGCTCTCAGGTTCAAAACCAAGCAGAGTTGATGTTGGTGAAG 240
DB 676 GCTTGATCTAAGGCTCTCAGGTTCAAAACCAAGCAGAGTTGATGTTGGTGAAG 617
QY 241 ACCTCAGAGACTTCTATCTTGTGTTATGATGATCAGATGTTCCAAAGTCTTACAC 300
DB 616 ACCTCAGAGACTTCTATCTTGTGTTATGATGATCAGATGTTCCAAAGTCTTACAC 557
QY 301 CTCACCTCCGAGAAATATCTCATTGTTGTTGATGATGATGATGATGATGATGATG 360
DB 556 CTCACCTCCGAGAAATATCTCATTGTTGTTGATGATGATGATGATGATGATGATG 497
QY 361 CCTTGGCAATGAGATGTTGTGTGACGAAATCCAAAGTCCCACTCAGAGAAATTCATG 420
DB 496 CCTTGGCAATGAGATGTTGTGTGACGAAATCCAAAGTCCCACTCAGAGAAATTCATG 437
QY 421 TCGTGTATTAATTTGTTGACAGCTTGGCAGCAAAAGTGTATGACACAGAGTGGCC 480
DB 436 TCGTGTATTAATTTGTTGACAGCTTGGCAGCAAAAGTGTATGACACAGAGTGGCC 377
QY 481 AGAAGCTCAACACGCGAGTTGTTGATGATCTCAATCTGGGCTTCCGTTGGCCGAG 540
DB 376 AGAAGCTCAACACGCGAGTTGTTGATGATCTCAATCTGGGCTTCCGTTGGCCGAG 317
QY 541 TTTTCTCAATTTGTCAGAGAGAGTGGCTCGGAGAAAGACTTTAGATGGCTTCTT 600
DB 316 TTTTCTCAATTTGTCAGAGAGAGTGGCTCGGAGAAAGACTTTAGATGGCTTCTT 257
QY 601 CCTTATTAACCAATTTGATGATCTGATGATGATGATGATGATGATGATGATGATG 660
DB 256 CCTTATTAACCAATTTGATGATCTGATGATGATGATGATGATGATGATGATGATG 197
QY 661 TTTAATAACCAATTTTATGATACGAGTAACGAACGTTGATGATGATGATGATGATG 720
DB 196 TTTAATAACCAATTTTATGATACGAGTAACGAACGTTGATGATGATGATGATGATG 137
QY 721 TATAAGTGTATTAATAAATGAGAGGGGAGAAATGAGATGTTTACTTATATAGTG 780
DB 136 TATAAGTGTATTAATAAATGAGAGGGGAGAAATGAGATGTTTACTTATATAGTG 77
QY 781 TGTATGCGATTAATTAATTAATCTACATGAATGAAGTGTATTAATTAATTAATTA 840
DB 76 TGTATGCGATTAATTAATTAATCTACATGAATGAAGTGTATTAATTAATTAATTA 17
QY 841 AAAAAAAAAAAGTCTGAG 856
DB 16 AAAAAAAAAAAGTCTGAG 1

LOCUS ARI48906 855 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 622530.
ACCESSION ARI48906
VERSION ARI48906.1 GI:15112996
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 855)
AUTHORS Weigel, D. and Kardailsky, I.
TITLE Flowering locus T (FT) and genetically modified plants having modulated flower development
JOURNAL Patent: US 622530-A 1 01-May-2001;
FEATURES Location/Qualifiers
source 1..855 /organism="unknown"
BASE COUNT 263 a 151 c 193 g 248 t
ORIGIN

Query Match 98.4%; Score 842.4; DB 6; Length 855;
Best Local Similarity 99.8%; Pred. No. 1.2e-188;
Matches 854; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 TCTAGACTAGTGTATCCCGGGCTGCGAGAAATCAGACAGAGTTGTTCAAGATCAA 60
DB 1 TCTAGAACTAGTGTATCCCGGGCTGCGAGAAATCAGACAGAGTTGTTCAAGATCAA 60
QY 61 AGATGCTATTAATTAAGAGACCCTTATAGTAAGCAGAGTTGTTGAGACGTTCTTG 120
DB 61 AGATGCTATTAATTAAGAGACCCTTATAGTAAGCAGAGTTGTTGAGACGTTCTTG 120
QY 121 ATCCGTTTAATAGATCAATCACTCTAAAGGTTACTTATGCGCAAGAGAGTGAATAG 180
DB 121 ATCCGTTTAATAGATCAATCACTCTAAAGGTTACTTATGCGCAAGAGAGTGAATAG 180
QY 181 GCTTGATCTAAGGCTCTCAGGTTCAAAACCAAGCAGAGTTGATGTTGGTGAAG 240
DB 181 GCTTGATCTAAGGCTCTCAGGTTCAAAACCAAGCAGAGTTGATGTTGGTGAAG 240
QY 241 ACCTCAGAGACTTCTATCTTGTGTTATGATGATCAGATGTTCCAAAGTCTTACAC 300
DB 241 ACCTCAGAGACTTCTATCTTGTGTTATGATGATCAGATGTTCCAAAGTCTTACAC 300
QY 301 CTCACCTCCGAGAAATATCTCATTGTTGTTGATGATGATGATGATGATGATGATG 360
DB 301 CTCACCTCCGAGAAATATCTCATTGTTGTTGATGATGATGATGATGATGATGATG 360
QY 361 CCTTGGCAATGAGATGTTGTGTGACGAAATCCAAAGTCCCACTCAGAGAAATTCATG 420
DB 361 CCTTGGCAATGAGATGTTGTGTGACGAAATCCAAAGTCCCACTCAGAGAAATTCATG 420
QY 421 TCGTGTATTAATTTGTTGACAGCTTGGCAGCAAAAGTGTATGACACAGAGTGGCC 480
DB 421 TCGTGTATTAATTTGTTGACAGCTTGGCAGCAAAAGTGTATGACACAGAGTGGCC 480
QY 481 AGAAGCTCAACACGCGAGTTGTTGATGATCTCAATCTGGGCTTCCGTTGGCCGAG 540
DB 481 AGAAGCTCAACACGCGAGTTGTTGATGATCTCAATCTGGGCTTCCGTTGGCCGAG 540
QY 541 TTTTCTCAATTTGTCAGAGAGAGTGGCTCGGAGAAAGACTTTAGATGGCTTCTT 600
DB 541 TTTTCTCAATTTGTCAGAGAGAGTGGCTCGGAGAAAGACTTTAGATGGCTTCTT 600
QY 601 CCTTATTAACCAATTTTATGATACGAGTAACGAACGTTGATGATGATGATGATGATG 660
DB 601 CCTTATTAACCAATTTTATGATACGAGTAACGAACGTTGATGATGATGATGATGATG 659
QY 661 TTTAATAACCAATTTTATGATACGAGTAACGAACGTTGATGATGATGATGATGATG 720
DB 660 TTTAATAACCAATTTTATGATACGAGTAACGAACGTTGATGATGATGATGATGATG 719
QY 721 TATAAGTGTATTAATAAATGAGAGGGGAGAAATGAGATGTTTACTTATATAGTG 780
DB 721 TATAAGTGTATTAATAAATGAGAGGGGAGAAATGAGATGTTTACTTATATAGTG 780

Db 720 TATAAGTGTGTAATAAATGAGAGGGGAGAAATGAGAGTGTATTACTATTATAGTG 779

QY 781 TGTGATCCGATTAATTAATTAATCTACATGAATGAAGTGTATTATTTAAAAAAA 840

Db 780 TGTGATCCGATTAATTAATTAATCTACATGAATGAAGTGTATTATTTAAAAAAA 839

QY 841 AAAAAAAAACTCGAG 856

Db 840 AAAAAAAAACTCGAG 855

RESULT 3

AB027504 864 bp mRNA linear PLN 26-FEB-2000

LOCUS Arabidopsis thaliana FT (FLOWERING LOCUS T) mRNA, complete cds.

DEFINITION AB027504

ACCESSION AB027504

VERSION AB027504.1 GI:4903011

KEYWORDS FT.

SOURCE Arabidopsis thaliana (strain: Landsberg er) cDNA to mRNA.

ORGANISM Arabidopsis thaliana

REFERENCE 1 (sites)

AUTHORS Kobayashi, Y., Kaya, H., Goto, K., Iwabuchi, M. and Araki, T.

TITLE A pair of related genes with antagonistic roles in mediating flowering signals

JOURNAL Science 286 (5446), 1960-1962 (1999)

MEDLINE 20050938

REFERENCE 2 (bases 1 to 864)

AUTHORS Araki, T. and Kobayashi, Y.

TITLE Direct Submission

JOURNAL Submitted (19-MAY-1999) Takashi Araki, Grad. School of Science, Kyoto University, Department of Botany, Division of Biological Sciences, Sakyo-ku, Kyoto, Kyoto 606-8502, Japan (E-mail: taraki@agr.bot.kyoto-u.ac.jp, Tel: 81-75-753-4136, Fax: 81-75-753-4141)

FEATURES

source

1. 864

location/Qualifiers

/organism="Arabidopsis thaliana"

/strain="Landsberg er"

/db_xref="taxon:3702"

/chromosome="1"

/map="90 cm on F5114"

/note="Corresponds to nucleotides 10511-10780, 11596-11657, 12371-12411, and 12536-13005 of F5114 (Accession Number AC001229)."

gene

1. 864

/gene="FT"

70. 597

/gene="FT"

/standard_name="FLOWERING LOCUS T"

/note="Induces flowering; loss-of-function mutation delays flowering similar to mammalian phosphatidylinositol binding protein (PEBP) and hippocampal cholinergic neurostimulating peptide (HCNP) precursor"

/codon_start=1

/product="FT"

/protein_id="BA077838.1"

/db_xref="GI:4903012"

/translation="MSINIRDPILIVSVGDVLDPENRSTLTAVTGQREVTGIDLRPSOVONKPREIGEDIDRNRYTLMDPDPVPSNPHRLRYLMLVYDIDATGTTTGNEIVCTENSPTAGIRHVVFILRQLGRQIVAPGWRQNTREFAITVNLGLPVAAV FYNQRESGGGHRL"

polya_signal

671. 675

/gene="FT"

BASE COUNT 284 a 149 c 185 g 246 t

ORIGIN

Query Match 93.4%; Score 799.6; DB 8; Length 864;

Best Local Similarity 99.5%; Pred. No. 1.5e-178;

Matches 802; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 45 GTTGTTCAGATCAAGATGCTATTAATTAAGAGACCTCTTATAGTAGAGATT 104

Db 52 GTTGTTCAGATCAAGATGCTATTAATTAAGAGACCTCTTATAGTAGAGATT 111

QY 105 GTTGAGAGAGCTTCTTGATCCGTTTAATAGATCAATCACTCAAGATTACTATGGCAA 164

Db 112 GTTGAGAGAGCTTCTTGATCCGTTTAATAGATCAATCACTCAAGATTACTATGGCAA 171

QY 165 AGAGAGTGACTAATGCGTTGGATCTAAGCGCTTCTCAGTTCAAAACAGCCAGATT 224

Db 172 AGAGAGTGACTAATGCGTTGGATCTAAGCGCTTCTCAGTTCAAAACAGCCAGATT 231

QY 225 GAGATGGTGAAGAGACCTCAGAACCTCTTAATCTTGGTATAGTGGATCCAGATT 284

Db 232 GAGATGGTGAAGAGACCTCAGAACCTCTTAATCTTGGTATAGTGGATCCAGATT 291

QY 285 CCAAGTCTTACCAACCTCAGAACCTCAGAACCTCAGAACCTCAGAACCTCAGAACCT 344

Db 292 CCAAGTCTTACCAACCTCAGAACCTCAGAACCTCAGAACCTCAGAACCTCAGAACCT 351

QY 345 GCTACACTGCAACACCTTTGGCAATGAGATTGTGTTCGAAATCCAGTCCACT 404

Db 352 GCTACACTGCAACACCTTTGGCAATGAGATTGTGTTCGAAATCCAGTCCACT 411

QY 405 GCAGGAATTCATCGTGTGTTTATATTTGTTGACAGCTTGGCAGGCAACAGTGTAT 464

Db 412 GCAGGAATTCATCGTGTGTTTATATTTGTTGACAGCTTGGCAGGCAACAGTGTAT 471

QY 465 GCACACAGGTGGCGCCAGAACCTTCAACACTGCGAGTTGCTGAGATCTACAACTCGGC 524

Db 472 GCACACAGGTGGCGCCAGAACCTTCAACACTGCGAGTTGCTGAGATCTACAACTCGGC 531

QY 525 CTTCGCGTGGCGCGAGTTTCTACAAATGTCAGAGGAGAGTGGCTGGGAGAGAGA 584

Db 532 CTTCGCGTGGCGCGAGTTTCTACAAATGTCAGAGGAGAGTGGCTGGGAGAGAGA 591

QY 585 CTTAGATGGCTCTCTCTTATTAACCAATGATATTCATCTGATGATTTATGC 644

Db 592 CTTAGATGGCTCTCTCTTATTAACCAATGATATTCATCTGATGATTTATGC 651

QY 645 ATCTATAGTATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 704

Db 652 ATCTATAGTATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 711

QY 705 CTATAGTGTCAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 764

Db 712 CTATAGTGTCAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 771

QY 765 TTTACTATATATAGTGTGATGCGATATTAATTAATTAATTAATTAATTAATTAAT 824

Db 772 TTTACTATATATAGTGTGATGCGATATTAATTAATTAATTAATTAATTAATTAAT 831

QY 825 ATTATATAAAAAAAAAAAAAA 850

Db 832 ATTATATAAAAAAAAAAAAAA 857

RESULT 4

AY065378 840 bp mRNA linear PLN 26-APR-2002

LOCUS Arabidopsis thaliana putative flowering signals mediating protein

DEFINITION FT (At1g95480) mRNA, complete cds.

ACCESSION AY065378

VERSION AY065378.1 GI:17529185

KEYWORDS FT. cDNA.

SOURCE Arabidopsis thaliana.

ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 840)

AUTHORS Yamada, K., Liu, S.-X., Sakano, H., Pham, P. K., Banh, J., Chung, M. K.,

Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L., Carinci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shim, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R., and Theologis, A.

Arabidopsis Full Length cDNA Clones

Unpublished

2 (bases 1 to 840)

Yamada, K., Ban, H., Chang, C.H., Chang, E., Dale, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Carinci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shim, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R., and Theologis, A.

TITLE
JOURNAL
COMMENT

Direct Submission

Submitted (04-DEC-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carinci, P., Kawai, J., Hayashizaki, Y., and Shinozaki, K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada, K., Ban, H., Chang, C.H., Chang, E., Dale, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Carinci, P., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shim, P., Southwick, A., Davis, R.W., Ecker, J.R., and Theologis, A.

Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.

FEATURES

source

Location/Qualifiers

1..840

/organism="Arabidopsis thaliana"

/db_xref="taxon:3702"

/chromosome="1"

/clone="RAFL06-80-B19 (R11796)"

/note="This clone is in a modified pBluescript vector (Lambda ZAP) as a XhoI/SstI insert."

ecotype: Columbia

1..840

/gene="Atlg65480"

1..82

/gene="Atlg65480"

83..610

/gene="Atlg65480"

/codon_start=1

/evidence="experimental"

/product="putative flowering signals mediating protein FT"

/protein_id="FAL38819.1"

/db_xref="GI:17529186"

/translation="MSINIRDPILVSRVGVDPNPSITLKYTGOREVTNGIDLR PSQVKNPRVEIGEDLRFNFTLVAVDPSVSPHRLVMDIPLPTGTGGS NEIYCENSPSTAGIHRVFTFLRQLGQTYVAGWQNGNFTREAEIYNGLPVAV FYNCRSGCGGRLL"

gene

5'UTR

CDS

3'UTR

BASE COUNT

ORIGIN

276 a 148 c 182 g 234 t

Query Match 89.2%; Score 763.4; DB 8; Length 840;

Best Local Similarity 99.2%; Pred. No. 5.4e-170;

Matches 767; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

45 GTTGTCAAGATCAAGTGTCTAATAATAGAGACCCCTTATAGTACGAGTT 104

|||||

Db 65 GTTGTTCAGATCAAGATGTCTAATAATAGAGACCCCTTATAGTACGAGTT 124

QY 105 GTTGGAGAGCTTCTGATCCGTTTAAATAGATCAATCACTCTAAAGTACTATGCGCAA 164

Db 125 GTTGGAGAGCTTCTGATCCGTTTAAATAGATCAATCACTCTAAAGTACTATGCGCAA 184

QY 165 AGAGAGAGTCAATAGCGTTGATCTAAGCGCTTCCAGGTTCAAAACAGCAGAGTT 224

Db 185 AGAGAGAGTCAATAGCGTTGATCTAAGCGCTTCCAGGTTCAAAACAGCAGAGTT 244

QY 225 GAGATTGGTGGAGAGAGAGTCAAGAGTCTTACTCTTGGTATGTTGATGATCAATGTT 284

Db 245 GAGATTGGTGGAGAGAGTCAAGAGTCTTACTCTTGGTATGTTGATGATCAATGTT 304

QY 285 CCAAGTCCAGAGAGAGTCAAGAGTCTTACTCTTGGTATGTTGATGATCAATGTT 344

Db 305 CCAAGTCCAGAGAGTCAAGAGTCTTACTCTTGGTATGTTGATGATCAATGTT 364

QY 345 GCTACAACTGGAACAACCTTTGGCAATGAGATTGTGTTCAGAAATCCAGTCCACT 404

Db 365 GCTACAACTGGAACAACCTTTGGCAATGAGATTGTGTTCAGAAATCCAGTCCACT 424

QY 405 GAGAGATTCATCGTCTGCTGTTTATGTTTTCAGACAGCTTGGAGGAGGAGGAGTAT 464

Db 425 GAGAGATTCATCGTCTGCTGTTTATGTTTTCAGACAGCTTGGAGGAGGAGGAGTAT 484

QY 465 GCACCAAGTGGCGCCGAGAACTTCAACACTCCGAGTTTGTGATCTACATCTCGGC 524

Db 485 GCACCAAGTGGCGCCGAGAACTTCAACACTCCGAGTTTGTGATCTACATCTCGGC 544

QY 525 GTTCCCGTGGCGCGAGTTTGTACAAATGTGAGAGGAGAGTGGCTGGGAGGAGGAG 584

Db 545 GTTCCCGTGGCGCGAGTTTGTACAAATGTGAGAGGAGAGTGGCTGGGAGGAGGAG 604

QY 585 CTTTGAAGTGGCTTCTTCCCTTATTAACCAATGATATGATCTGATGAGATTTATGC 644

Db 605 CTTTGAAGTGGCTTCTTCCCTTATTAACCAATGATATGATCTGATGAGATTTATGC 664

QY 645 AACTATAGTATTTTATTTAATTAACATTTTATGATGATGATGATGATGATGATG 704

Db 665 AACTATAGTATTTTATTTAATTAACATTTTATGATGATGATGATGATGATGATG 724

QY 705 CATAGTACTTCAATATATTAATGATGATGATGATGATGATGATGATGATGATG 764

Db 725 CATAGTACTTCAATATATTAATGATGATGATGATGATGATGATGATGATGATG 784

QY 765 TTTTACTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 817

Db 785 TTTTACTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 837

RESULT 5

AB027505 780 bp mRNA linear PLN 26-FEB-2000

LOCUS

DEFINITION Arabidopsis thaliana FT (FLOWERING LOCUS T) mRNA, complete cds,

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana (strain Landsberg er) cDNA to mRNA.

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

Direct Submission

Araki, T. and Kobayashi, Y.

JOURNAL Submitted (19-MAY-1999) Takashi Araki, Grad. School of Science,
Kyoto University, Department of Botany, Division of Biological
Sciences, Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
(E-mail: taraki@gr.bot.kyoto-u.ac.jp, Tel: 81-75-753-4136,
Fax: 81-75-753-4141)

FEATURES

source

Location/Qualifiers
1. /780
/organism="Arabidopsis thaliana"
/strain="Landsberg er"
/db_xref="taxon:3702"

/note="Corresponds to nucleotide 10511-10780,
11596-11657, 12371-12411, and 12536-13005 of F5114
(Accession Number AC001229)"

gene

1. /780
/gene="FT"
70. /438
/gene="FT"
/standard_name="FLOWERING LOCUS T"
/note="amino acid residues 1-101 of hypothetical
translation product are identical to those of FT protein
detected in two ecotypes examined, Landsberg er and
Columbia
first 77 bases of the fourth exon of FT are lacking due to
alternative splice acceptor site"
/codon_start=1
/product="FT"
/protein_id="BA77839.1"
/db_xref="GI:4903014"
/translation="MSINIRDLPLVSRVVDVLDPPNRSITLKVYRGOREVTGLDLR
PSOVOKRPRVEIGEDLRNFYTLVWDPVPSNPDLREYLMVTDLPATGTTF
MOANSYCTVAPLEHSRVC"

CDS

BASE COUNT 257 a 135 c 167 g 221 t
ORIGIN

Query Match 74.3%; Score 635.6; DB 8; Length 780;
Best Local Similarity 90.0%; Pred. No. 8.7e-140;
Matches 725; Conservative 0; Mismatches 4; Indels 77; Gaps 1;

45 GTTGTTCAGATCAAGAAGTCTATTAATTAAGACACCTCTTAATAGTACAGAGTT 104
|||||
52 GTTGTTCAGATCAAGAAGTCTATTAATTAAGACACCTCTTAATAGTACAGAGTT 111
|||||
105 GTTGTTCAGATCAAGAAGTCTATTAATTAAGACACCTCTTAATAGTACAGAGTT 164
|||||
112 GTTGTTCAGATCAAGAAGTCTATTAATTAAGACACCTCTTAATAGTACAGAGTT 171
|||||
165 AGAGAGTACTAATGCTTGATCTAAGGCTTCTCAGGTTCAAAACCAAGCAAGATT 224
|||||
172 AGAGAGTACTAATGCTTGATCTAAGGCTTCTCAGGTTCAAAACCAAGCAAGATT 231
|||||
225 GATATTGCTGGAAGACCTCAGAGACTCTTATCTTTGGTTATGTTGATCCAGATGTT 284
|||||
232 GATATTGCTGGAAGACCTCAGAGACTCTTATCTTTGGTTATGTTGATCCAGATGTT 291
|||||
285 CCAAGTCTCAGACACCTCTCAGCTCCGAGATATCTCCATGGTTGGTATGATATCCCT 344
|||||
292 CCAAGTCTCAGACACCTCTCAGCTCCGAGATATCTCCATGGTTGGTATGATATCCCT 351
|||||
345 GCTACAACCTGGAACCAACCTTTGGCAATGAGATTGTGTACGAAAAATCCAAAGTCCACT 404
|||||
352 GCTACAACCTGGAACCAACCTTT----- 372
|||||
405 GCAGGAATTATGCTGTGCTGTTTATATTTGTTTCGACAGCTGGCAGGCAAAAGTAT 464
|||||
373 -----GCTTGGCAGGCAAAAGTAT 394
|||||
465 GCACAGAGGTGGCGCCAGAACTTCAACACTGCGAGTTGCTGATCTCAATCTGGGC 524
|||||
395 GCACAGAGGTGGCGCCAGAACTTCAACACTGCGAGTTGCTGATCTCAATCTGGGC 454
|||||
525 CTTCCCGTGGCGCAGATTCTCAATTTGTACAGAGGAGAGAGTGGCTGCGAGGAAGAGA 584
|||||
455 CTTCCCGTGGCGCAGATTCTCAATTTGTACAGAGGAGAGAGTGGCTGCGAGGAAGAGA 514
Db

QY 585 CTTAGATGGCTTCTCTCTTATATACCAATGATATGCACTCTGATGAGATTATGC 644
|||||
Db 515 CTTAGATGGCTTCTCTCTTATATACCAATGATATGCACTCTGATGAGATTATGC 574
|||||
QY 645 ATCTATAGTATTTTAATTAATAACATTTTATGATACGATACGAACGGTGATGATGC 704
|||||
Db 575 ATCTATAGTATTTTAATTAATAACATTTTATGATACGATACGAACGGTGATGATGC 634
|||||
QY 705 CTATAGTATGTCATATATAGTGTGTAATTAATAAGAGGGGAGGAAATATAGATGC 764
|||||
Db 635 CTATAGTATGTCATATATAGTGTGTAATTAATAAGAGGGGAGGAAATATAGATGC 694
|||||
QY 765 TTTTACTTATATAGTGTGATGCGATATATATATATATATATATATATATATATAT 824
|||||
Db 695 TTTTACTTATATAGTGTGATGCGATATATATATATATATATATATATATATATAT 754
|||||
QY 825 ATTAT 850
|||||
Db 755 ATTAT 780
|||||

RESULT 6
LOCUS AY133813
DEFINITION Arabidopsis thaliana clone U11796 putative flowering signals.
ACCESSION AY133813 GI:22136805
VERSION AY133813.1
KEYWORDS FT, CDS.
SOURCE Arabidopsis thaliana.
ORGANISM Arabidopsis thaliana.

REFERENCE
AUTHORS
1 (bases 1 to 559)
Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Deng, J.M., Hsuan, V.W.,
Lee, J.M., Quach, H.L., Tang, C.C., Toriumi, M., Wallender, E.K.,
Wong, C., Wu, H.C., Yu, G., Yuan, S., Bower, L., Carninci, P., Chen, H.,
Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A.,
Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M.,
Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M.,
Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.
Arabidopsis Open Reading Frame (ORF) clones

TITLE
JOURNAL
REFERENCE
AUTHORS
Unpublished
2 (bases 1 to 559)
Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Deng, J.M., Hsuan, V.W.,
Lee, J.M., Quach, H.L., Tang, C.C., Toriumi, M., Wallender, E.K.,
Wong, C., Wu, H.C., Yu, G., Yuan, S., Bower, L., Carninci, P., Chen, H.,
Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A.,
Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M.,
Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M.,
Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and
Theologis, A.

TITLE
JOURNAL
COMMENT
Submitted (17-JUL-2002) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
The RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAPD cDNAs (RAPD cDNA: 'RIKEN
Arabidopsis Full-Length cDNA'): Seki, M., Narusaka, M., Ishida, J.,
Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PSEC (SSP) Consortium members constructed and
sequenced the PUNI (ORF) clones using the RAPD cDNAs: Yamada, K.,
Chan, M.M., Chang, C.H., Dale, J.M., Deng, J.M., Hsuan, V.W., Lee, J.M.,
Quach, H.L., Tang, C.C., Toriumi, M., Wallender, E.K., Wong, C.,
Wu, H.C., Yu, G., Yuan, S., Bower, L., Chen, H., Cheuk, R., Jones, T.,
Karlin-Neumann, G., Kim, C., Lam, B., Lin, J., Miranda, M., Nguyen, M.,
Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and
Theologis, A.

Yamada, K. (SSP/PSEC) and Seki, M. (RIKEN GSC) contributed equally

LL118r"

complement(47061. .49870)

/gene="F5114.8"

complement(join(47061. .47422,47541. .47632,47766. .47824,47929. .48015,48122. .48218,48340. .48525,48704. .48799,48884. .48959,49053. .49153,49242. .49418,49467. .49532,49587. .49654,49750. .49870))

/gene="F5114.8"

/note="Similar to Zea mays permease 1 (gb|U043034)." /codon_start=1

/evidence=not_experimental

/protein_id="AAB60909.1"

/db_xref="GI:2190545"

/translation="MTNGGGGNGGNAANRTEELQPHRYKQLPEIQIVNSPPMLEAVVLGFRVHLISLIVLIPMLTEFFFEFFFLNRRESILLFYAKRNVQITLEVSGLTTLFQSEFTIRLVAVASAVYIPIISLIYRFLVYHGFPEFYVMQMSIQCALITGCEVFLILGVNRVIRPLSLPLATFGLYHGHGFLFVYHGMQISFIPOLARCEVLPGLIILITFYQYLPRLKLNKGMIIIDPDSRCDRGMTICLPIWLFQQLTSSGVYDKHSHHTYQTSRDTBTLGILTNPMWYIIPYFPMQSPETIDTDSFAMMAVYLFESTLFPASAVGSGATPIPPSVSRGTCTMAGVGLVNLMLGDTITSTENVGILAMTKIGSRVIRIOLSAFMFIEFISFGFGAFASIPPIPMASLVCIVLFCFSFSHHICSAIEINCFIEFFFKINSYIYNASVGLSYLQFCNLNSFNKIFILGFSFMAISIPDYFRFYVNGMRSHDSNMVSYSTLL"

complement(50678. .52743)

/gene="F5114.9"

complement(join(50678. .51059,51406. .51488,51567. .51733,51818. .52033,52078. .52294,52510. .52743))

/gene="F5114.9"

/note="Strong similarity to Arabidopsis zeta-crystallin-like protein (gb|Z49268)." /codon_start=1

/evidence=not_experimental

/protein_id="AAB60917.1"

/db_xref="GI:2190553"

/translation="MGEVSYVENKRVILKNYVDGILPEIDMEYKLGFTIELKAPKSSCLFLVKNLLISCDPIRGRGRDHDHGSYLPRPVGQKCEVLRYVLFGLFTFEERBCVCIYALRSRCSPPRCDEKRWYMLKLEICYILVKKLTFEINSLITDSVFLMRCRIEGLARVITDSDTNGPVGIVGIIEMEYSLRSDINLOLRDLDLPIYHGLIGLMAEFTVAGSNEICPKPKSGVSAACGAVGOLVGLARHGCVVGSAGSKGRVIALKNEGLDYEMFANKEEDLDTALKRPRPEGIDITYDVNGSGMLDALLNMKVRGRVIALCVSLQSLSTSSOGINKLNSAIYTKRRLBSFDLSDYLIHFPQPLENKRYYKEKIVYVDSISBDLAPALVGLFSGKNIGQVRYKARE"

complement(53168. .54916)

/gene="F5114.10"

complement(join(53168. .53386,53596. .54114,54461. .54916)/gene="F5114.10"

/note="Strong similarity to Solanum polygalacturonase precursor (gb|U23053)." /codon_start=1

/product="F5114.10"

/protein_id="AAB60920.1"

/db_xref="GI:2190556"

/translation="WALTLSEVQFSIVYITIMSHFGQDARTSLNLSFGANPNCIVESAPDAMPACQCEVDSYIVYKGRVLVSGEAFEESSCRSEITRLRIDTLTGPODYSLILGKEMNFSFQVYHNVVLGSGSVCYSFACSCANQVCEGATLFEQMSNVKIKLGLKSLNSQFVGLIINRCNRKIDEVRIIADPESNTGIIHOLSTLIEVRASITKDDQDSTIDPGKNLVAVDGLTGARGHISGLAKSIEBQGVENVYKNAVYVTDNLGRKMPRNSNGEVYRFLGAILMVNVSTPITLIDNTCPDSDSPQSDSGKIDVYISLIGMSISAEIALKMDQSEKVPQGTGRIMQVITLIDNTSYEAKTSTCTNSGQGLGIVT

Query Match 54.4%; Score 466; DB 8; Length 109560;
Best Local Similarity 100.0%; Pred. No. 8.3e-100;
Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

366 GGCAATGAGATTGTGTTACGAAATCCAAGTCCCACTGCAGGAATCATCGTCTG

Db 12535 GGCAATGAGATTGTGTGTACGAAATCCAAGTCCCACTGCAGGAATTCATCGTCTG

426 TTTATATTGTTTCGACAGCTTGGCAGGCAACAGTGTATGCACCAGGGTGGCCGACGAAC

Db 12595 TTTATATTGTTTCGACAGCTTGGCAGGCAACACAGTGTATGCACCAGGTTGGCGCAGAAC 12654

OY	466	TTCAACACTGCGAGTTTGCTGTAGATCTACATCTCCGCGTTCCCGGCGGAGTTTC	545
Db	12655	TTCAACACTGCGAGTTTGCTGTAGATCTCAATCTCCGCGTTCCCGGCGGAGTTTC	12711
OY	546	TACAAATGTCAGAGGAGAGTGGCTGCGGAGAGACATTTAGATGGCTTCTCCCTT	605
Db	12715	TACAAATGTCAGAGGAGAGTGGCTGCGGAGAGACATTTAGATGGCTTCTCCCTT	12774
OY	606	ATAACCAATTCGATTTGCACTCTCATGATGATTTATGCACTTATGATTTTAAATTAA	665
Db	12775	ATAACCAATTCGATTTGCACTCTCATGATGATTTATGCACTTATGATTTTAAATTAA	12833
OY	666	TAAACATTTTATGATACAGTAAACGAGGTATGATGCTTATAGTAGTTCAATATTAA	725
Db	12835	TAAACATTTTATGATACAGTAAACGAGGTATGATGCTTATAGTAGTTCAATATTAA	12894
OY	726	GTCGTAAATAAATGAGAGGGGAGAAATGAGAAGTGTCTTACTTATATAGTGTGTA	785
Db	12895	GTCGTAAATAAATGAGAGGGGAGAAATGAGAAGTGTCTTACTTATATAGTGTGTA	12954
OY	786	TGCATATATATATATATCTACATGAAAGAGCTTATATTATTAA 831	
Db	12955	TGCATATATATATATATCTACATGAAAGAGCTTATATTATTAA 13000	

RESULT 9	LOCUS	2483 bp	DNA	linear	PLN 22-DEC-1999
AF152096	Arbidiopsis thaliana flowering locus T (FT) gene, complete cds.				
DEFINITION	Arbidiopsis thaliana flowering locus T (FT) gene, complete cds.				
ACCESSION	AF152096				
VERSION	AF152096.1				GI:6117977

ORGANISM

REFERENCE
AUTHORS
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:
Rosidae: eucosids II: Brassicales: Brassicaceae: Arabidopsis.
1 (bases 1 to 2463)
Kardailsky, I., Shukla, V. K., Ahn, J. H., Degenals, N.,

TITLE	Activation tagging of the floral inducer FT
JOURNAL	Science 286 (5446), 1962-1965 (1999)
MEDLINE	20050959
PUBMED	10583961
REFERENCE	2 (Bases 1 to 2483)
AUTHORS	Kardalisky, I. and Weigel, D.
TITLE	Direct Submission
JOURNAL	Submitted (17-MAY-1999) Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, Jolla, CA 92037, USA

Source

```

/organism="Arabidopsis thaliana"
/cultivar="Col umbria"

```

```

/db_xref="taxon:3702"

```

```

/chromosome="I"
/mao="90 CM: F5T1A"

```

gene 1. :2483

gene="PT"	364	1080	1141	1855	1895	2020	2483
MBNA	401	1	1	1	1	1	1

```

join(1: 2004, 10000: 11141, 10000: 11141, 10000: 11141)
/gene="FT"

```

```

1  /product="flowering locus T"
2  E1/rmp

```

```

    2 01K
    .1, .03
    /gene="FT"

```

```
CDS      join(64. .264,1080. .1141,1855. .1895,2020. .2243)
```

```
/gene="F1"
/function="induces flowering"
```

/note="similar to hippocampal cholinergic neurostimulating

peptide (HCNP) precursor, phosphatidylinositolamine protein (PEBP) and Raf kinase inhibitor protein?

corresponds to *Arabidopsis thaliana* BAC F5114 sequence

[illegible]

RESULT 11					
LOCUS	AF152907	528 bp	mRNA	linear	PLN 22-DEC-1999
DEFINITION	Arabidopsis thaliana twin sister of FT (TSF) mRNA, complete cds.				
ACCESSION	AF152907				
VERSION	AF152907.1	GI:6117979			

SOURCE ORGANISM	Arabidopsis thaliana	Arabidopsis thaliana
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
28	28	28
29	29	29
30	30	30
31	31	31
32	32	32
33	33	33
34	34	34
35	35	35
36	36	36
37	37	37
38	38	38
39	39	39
40	40	40
41	41	41
42	42	42
43	43	43
44	44	44
45	45	45
46	46	46
47	47	47
48	48	48
49	49	49
50	50	50
51	51	51
52	52	52
53	53	53
54	54	54
55	55	55
56	56	56
57	57	57
58	58	58
59	59	59
60	60	60
61	61	61
62	62	62
63	63	63
64	64	64
65	65	65
66	66	66
67	67	67
68	68	68
69	69	69
70	70	70
71	71	71
72	72	72
73	73	73
74	74	74
75	75	75
76	76	76
77	77	77
78	78	78
79	79	79
80	80	80
81	81	81
82	82	82
83	83	83
84	84	84
85	85	85
86	86	86
87	87	87
88	88	88
89	89	89
90	90	90
91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

REFERENCE

Kardail'sky, I., Shukla, V. K., Ahn, J. H., Degenals, N.,
Kardail'sky, I.

Christensen, S. K., Nguyen, J. T., Chory, J., Harrison, M. J., and Weigel, D.
Activation tagging of the floral inducer *FT*
Science 286 (5446), 1962-1965 (1999)
20050959

10583961
 2 (bases 1 to 528)
 Haaksma, S., Shukla, V.K., Ahn, J.H. and Welgel, D.

TITLE Direct Submission
JOURNAL Submitted (19-MAY-1999) Plant Biology Laboratory, The Salk
Institute for Biological Studies, 10010 N. Torrey Pines Road, La
Jolla, CA 92037, USA

FEATURES	Location/Qualifiers
source	1. .528

```

/organism="Arabidopsis thaliana"
/cultivar="Columbia"
/db_xref="taxon:3702"
/chromosome="IV"
/map="between g3883 and g13838"
1..528

```

	/gene="TSF"
CDS	1. .528

/gene="TSF"
/note="flowering locus T (FT) homolog; similar to
hippocampal cholinergic neurostimulating peptide (HCNP)
precursor, phosphatidylethanolamine binding protein (PEBP)
and Raf kinase inhibitor protein"
/codon_start=1

```

/product="twin sister of Ft
/protein_id="AA03937.1"
/db_xref="GI:6117980"
/translation="MSLSRRDPLVVGSGVDLDPFTWRIVSLKTYGHEVTNGIDLRL
PSQVINKDIVEIGSDDEPRNFETLVMDVDPSGPNQRDELHLVMDIPATTCNAFQ
NSVQCYSPRPSSILHRILVLFKQLQRYIAFGWKQQTPTREAFELIYNGLPAVAS
YFNCQRENGCGGKRT".

```

BASE COUNT	123	A	116	C	142	G	14	T
ORIGIN								

Query Match	44.1%	Score 377.6:	DB 8:	Length 528;
Best Local Similarity	82.2%	Pred. No. 8.3e-79;		
Matches 434; Conservative	0;	Mismatches 94;	Indels 0;	Gaps 0;

63 ATGCTATAAATATAAGAGACCCCTTATAGTAAGCAGAGTTGTTGGAGACGTTCTTGAT 122

123 CCGTTTAATGATCAATCAATCTCTAABGCGTAACTTAAATGGCCCAAAAGACAGCTGACAAATCCC 1822
Dd 1 ATGCTTTAAGTCGAGAGATCCCTCTGTGGTGGCGCAGTGTCTTTGGAGATGATCTTGTAT 60

61 CCTTTCACGAGTTGGTCTCTTAAGTCACTTATGCGCCATAGAGAGTTACTAATGCG 120

Accession	Sequence	Position
QY	TTGGATCTTAAGCCCTTTCACAGTTCAAAACCAAGCCAGATGTGGATGTGGTGGGAAGAC	24.2
Db	TTGGATCTTAAGCCCTTTCACAGTTCTGAACAAACCAATATGGAGATTTGGAGGAGACAC	180
QY	CTCAGGAACCTCTTACTTTTGGTATATGTGTGATCTCAAGATGTTCACAGTCTTACGACACCT	30.2
Db	CTCAGGAACCTCTTACTTTTGGTATATGTGTGATCTCAAGATGTTCACAGTCTTACGACACCT	240

QY 303 CACCTCCGAGATATCTCCATGTGTGGTGA CTGATATCCCTGCTACAACTGGACACACC 362
|||||

Db 241 CACCAACGAGATATCTCCACTGGTTGGTGCATGATATACCTGCCACCACTGGAATGcc 300

Db 301 TTTGGCATTGAGCTGGTGTCTACGAGAGTCCACGTCCTCCCTCGGGGAAATTATCGTATT 360

423 GTGTTTATATGTTTCGACAGCTGGCAGGCCAAACAGTGTATGACACCAAGGGTGGCCAG 482

Db 361 GGTGTGTTATGTTCCGGCACTCGGAGACAMACGGTTTATGCAACCGGGGTGGCCAA 420

Db

	483	ACTTCACACATCGGAGTTTGTCTGAGATCTACAAATCTGGCCCTCCGCGGCAGCT	542
OY			
	421	CAGTTCAACACTCGTAGTTTGCTGAGATCTACAATCTTGGTCTTCCTGTGGCTGCCCTC	480

OY 543 TTCTACAAATTGTCAGAGGAGAGTGGCTGCGGAGAGAAGACTTTAG 590

Db 481 TACTTCAACTGCCAGAGGGAATGGCTGTGGGGGAAGAAGACCTAG 528

RESULT 12
E38986

LOCUS	528 bp	DNA	linear	PAT 31-JAN
E38986	Method	for shortening plant generation and plant.		
000000	Accession			

ACCESSION E56986
VERSION E38986.1 GI:18625005
KEYWORDS JP 2000139250-A/2.

SOURCE Arabidopsis.
ORGANISM Arabidopsis
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta

spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae.

REFERENCE
AUTHORS
TITLE

1 (bases 1 to 526)
Araki, T., Kobayashi, K., Ogawa, K. and Shirai, M.
Method for shortening plant generation and plant

COMMENT
OS Arabidopsis
TORAY IND INC
Patent: JP 2000139250-A 2 23-MAY-2000;
.JOURNAL

PD 23-MAY-2000
 PD 11-NOV-2000 TD 1000000000
 PN JP 2000139250-A/2
 PD 23-MAY-2000

PI	11-NOV-1998	JP	1998320219
PR			
PF			
TA			
AK			
SH			
IR			
RA			
KA			
OG			
MA			
KO			
YO			
SH			
IR			
AR			
AK			
RA			
KA			
OG			
MA			
KO			
YO			
SH			
IR			
RA			
KA			
OG			
MA			
KO			
YO			
SH			
IR			
RA			
KA			
OG			
MA			
KO			
YO			
SH			
IR			
RA			
KA			
OG			
MA			
KO			
YO			
SH			
IR			
RA			
KA			
OG			
MA			
KO			
YO			
SH			
IR			
RA			
KA			
OG			
MA			
KO			
YO			
SH			
IR			
RA			
KA			
OG			
MA			
KO			
YO			
SH			
IR			
RA			
KA			
OG			
MA			
KO			
YO			
SH			
IR			
RA			
KA			
OG			
MA			
KO			
YO			
SH			
IR			
RA			
KA			
OG			
MA			
KO			
YO			
SH			
IR			
RA			
KA			
OG			
MA			
KO			
YO			
SH			
IR			
RA			
KA			
OG			
MA			
KO			
YO			
SH			
IR			
RA			
KA			
OG			
MA			
KO			
YO			
SH			
IR			
RA			
KA			
OG			
MA			
KO			
YO			
SH			
IR			
RA			
KA			
OG			
MA			
KO			
YO			
SH			
IR			
RA			
KA			
OG			
MA			
KO			
YO			
SH			
IR			
RA			
KA			
OG			
MA			
KO			
YO			
SH			
IR			
RA			
KA			
OG			
MA			
KO			
YO			
SH			
IR			
RA			
KA			
OG			
MA			
KO			
YO			
SH			
IR			
RA			
KA			
OG			
MA			
KO			
YO			
SH			
IR			
RA			
KA			
OG			
MA			
KO			
YO			
SH			
IR			

A01H1/00, A01H5/00, C12N5/10, C12N15/09/((C12N5/10, C12R1:91), PC (C12N15/09, C12R1:91), C12N5/00, C12N15/00, (C12N5/00, C12R1:91), P (C12N15/00, C12R1:91))

Key	Location/Qualifiers
CC	
EH	
FM	

FT, source	1. .528
FT	/organism='Arabidopsis',
FEATURES	Location/Qualifiers

```
source
1. 528
/organism="Arabidopsis"
/chr="chr1"
/chr_start="1701"
/chr_end="1701"
```

BASE COUNT	122	a	117	c	142	g	147	t
ORIGIN								

Query Match	43.7%	Score 374.4;	DB 6;	Length 528;
Best local Similarity	81.8%;	Pred. No. 4.7e-78;		

Matches	432	Conservative	0	Mismatches	96	Indels	0	Gaps	0
---------	-----	--------------	---	------------	----	--------	---	------	---

Db 1 ATGCTTTAAGTCGTAGAGATCCCTCTCGTGGCAGTGTTCTTGAGAGATGTTCTTGAT 60

OY	123	CGGTTATATACATCAATCAGCTTAAAGGTTCATTATGGCCAAAGAGAGACTAATAAGGC	182
Db	61	CCTTTCACAGAGGTGGTGCTCTCTTAAGGTCACTTATGGCCATAGAGAGTTACTTAATGGC	120
OY	183	TTTGATCTAAGGCCCTTCTCAGGTTCAAACAAGCCAAAGTAGTTGAGTTGGTGAGAACAC	242
Db	121	TTGGATCTAAAGGCCCTTCTCAAGTTCTGTAAACAACAACCAATAGTGAATTTGAGAGAGACAC	180
OY	243	CTCAGGAACCTCTAATCTTTGGTATGGTGGATCCAGATGTTCCAAGTCTAGCAACCCT	302
Db	181	TTCAAAAATTTCTCACCTGGTATGGTGAATCTGTATGGCGAAGCCAAAGAACCCT	240
OY	303	CACCTCCGAGATATCTCCATTTGGTTGGTGCATGATATCCCTGCATACACAGAACACAC	362
Db	241	CACCAAGAGAAATCTCCACTGTTGGTGAATCATATNACTGGCCACACATCGAAAAATGCC	300
OY	363	TTTTGGCAATGAGANTGTGTGTATACGAAAATCCAAAGTCCCACATGCAGGAATTCATGTGTC	422
Db	301	TTTTGGCAATGAGGTGGTGCTGTACGAGAGTCCAGGTCCCCCTCGGGGAATTCATGTGATTT	360
OY	423	GGTATTATATGTTCGACAGCTGGCGAGGAAACAGTGTATGGACGAGGGGTGGGCGCAG	482
Db	361	GTGTTGGATGTGTTCGCGCAACTCGGAAGACAAACGGTTTATGCCACGGGGTGGCGCATA	420
OY	483	AAC TTC AAC ACT CG GAG GTT TGT CAG AT CT CA A TC TG G C C TT CC G TG G C C G C AG TT	542
Db	421	CAGTTCACACTCGGATGATTTGCTGAGATCTACAATCTTGSTCTTCCTGGTGCCCTCT	480
OY	543	TTTCAACAATTCGAGAGGAGAGTGGCTGGCGAGGAANAACAACTTTAC	590
Db	481	TACTTCAACTCCAGAGGAGGAATAAGCGTGTGGGGGAANAACAACCTTAC	578

AB027456	RESULT 13
LOCUS	
AB027456	
DEFINITION	AB027456 745 bp mRNA . linear PLN 26-FEB-2000
ACCESSION	AB027456
VERSION	AB027456.1 GI:4903138
KEYWORDS	CITF.
SOURCE	Citrus unshiu (strain: Miyagawa-wase satsuma mandarin) developing stage juice sac and pulp segment cDNA to mRNA.
ORGANISM	Citrus unshiu
REFERENCE	Eukaryotes: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eucotids II; Sapindales; Rutaceae; Citrus.
AUTHORS	1 (sites)
TITLE	Kobayashi, Y., Kaya, H., Goto, K., Iwabuchi, M. and Arai, T.
JOURNAL	A pair of related genes with antagonistic roles in mediating flowering signals
MEDLINE	Science 286 (5446), 1960-1962 (1999)
REFERENCE	20050958
AUTHORS	2 (bases 1 to 745)
TITLE	Omura, M., Kobayashi, Y. and Arai, T.
JOURNAL	Direct Submission
FEATURES	Submitted (17-MAY-1999) Mitsuo Omura, National Institute of Fruit Tree Science, Department of Citriculture, Okitsu, Shimizu, Shizuoka 424-0292, Japan (E-mail:om9330@okt.affrc.go.jp, Tel:81-543-69-7108, Fax:81-543-69-2115)
source	Location/Qualifiers
	1..745

```

gene      1.7A5
          /gene="ClFT"
CDS       96..629
          /gene="ClFT"
          /note="extensive homology to FT (FLOWERING LOCUS T

```

BASE COUNT	ORIGIN
195 a	AB027504) and tsf (TWIN SISTER OF FT, AB027506) genes of
150 c	Arabidopsis thaliana
180 g	similar to mammalian phosphatidylethanolamine binding
220 t	protein (PEBP) and hippocampal cholinergic
	neurostimulating peptide (HCNP) precursor"
	/codon_start=1
	/protein_id="BAA7836.1"
	/db_xref="GI:4903139"
	/translation="MSRRDPLVGRVGDVDLNFRTIPMTTYSNKNVNGRELK
	SEVLNQPAEIGDGLRTFTYLVMPDPAESPSPDLREYLVHLYVDIPATGASG
	OEIYNTESPRPTGTHRFVFLPQDLQRTGYVAGQWQNSITDFALNMGPPVAAV
	YFNQRRSGSGGPRYR"

Query Match	33.8%	Score 289.6	DB 8	Length 745
Best Local Similarity	72.3%	Pred. No. 5	1e-58	
Matches	376	Conservative	0	Mismatches 144; Indels 0; Gaps 0
QY	61	AGATGCTATATAATAAAGAGACCCCTCTTATAGTACGAGAGTGTGGAGACGTTCTTG	120	
Db	94	ATATGCTTAGCAGAGGAGAGAGATCCCTTATTTGTTGGCCGGTGTGTGATGTTCTTG	153	
QY	121	ATCCGTTAATATGATCATCTACTTAAGGTGTACTATGCGCAAGACAGTGTACTATG	180	
Db	154	ACAATTATTACAAAGAAACAAATCCAAAGAGAGATTACTATTAACAAAGAGATGTTAATATG	213	
QY	181	GCTTGGATCTAAGGCGCTCTCAGGTCTCAAAACAAAGCCAAAGATTGAGATTTGGTGAGAG	240	
Db	214	GCCGAGACTCAAACTCTGAGTTCGTAACACAGCCCTAGGGCTGAATTTGGTGTATG	273	
QY	241	ACCTCAGCACTCTATACCTTGGTTATGTTGATGCCAGATGTTCCAAAGCTCTAGCAAC	300	
Db	274	ATCTTAGAGCAATTTTATCTTTGGTAAAGGTTGATCTTGATGACCAACCAAGTGAAC	333	
QY	301	CTCACCTCGGAATATATCCATGGTGGTGAGTATATCCCTCACTCACTGSAACGA	360	
Db	334	CCAGCTTAGGAGATTTATTTGCTTGGTGGTACTGATATTCACAAACACAGGGGCCA	393	
QY	361	CTTGTGGCAATGAGATTTGTGTGTCGAATAATCCAAAGTCCACATCAGAAATTCATCTG	420	
Db	394	GCTTTGGCCAGAGATTTGTGAACATGAAAGCCCTAGGCCAAGATGGGANTTCACAGT	453	
QY	421	TCGTGTTAATATTTGTTGCAGACGCTTGCCAGGCAAAAGTGTATGACACAGGTTGGCC	480	
Db	454	TTGTCTTTGTGTGTCCGGCAACTTGGGAGGCAACACTGTTATACACAGGTTGGCC	513	
QY	481	AGAACTTCAACACTGGCAGTTTCTGTAGATCTAATATCTGGCCTTCCCGTGGCCGAG	540	
Db	514	AGAACTTCAGACGAGGAGATTTTGTGTGACTTTACAAATCTGGGACCTCCGGTGGCCGCTG	573	
QY	541	TTTTTACAAATTTGTGAGAGGAGAGTGTGCTGGCGAGAG	580	
Db	574	TCTACTTCACTGCCAGAGGAGGAGCGGATTCGGCGGAG	613	

RESULT 14

AX478001

LOCUS AX478001 899 bp DNA linear PAT 12-NOV-2002

DEFINITION Sequence 11 from Patent WO0244390.

ACCESSION AX478001

VERSION AX478001.1 GI:22217011

KEYWORDS

SOURCE

ORGANISM

Zea mays.

Zea mays.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC Clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

AUTHORS Calhoun, E.B., Calhoun, R.E., Klein, T.M., Rafalski, A.J. and Sakai, H.

TITLE Floral development genes.

JOURNAL Patent: WO 0244390-A 11 06-JUN-2002; E. I. du Pont de Nemours and Company (US)

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 2, 2003, 02:33:53 ; Search time 282.5 Seconds

(without alignments)
6823.754 Million cell updates/sec

Title: US-09-845-849-1

Perfect score: 856
Sequence: 1 tctagaactagtgtgctcccc.....aaaaaaaaaaaaactcgag 856

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

N.Geneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	856	100.0	856	AAZ28490	Flowering locus T
2	856	100.0	856	AAZ28491	Flowering locus T
3	692.4	80.9	775	AAZ28491	Flowering locus T
4	692	80.8	754	AAZ28491	Flowering locus T
5	528	61.7	528	AAZ28491	Flowering locus T
6	377.6	44.1	528	AAZ28491	Flowering locus T
7	374.4	43.7	528	AAZ28491	Flowering locus T
8	180.2	21.1	22	AAZ28491	Flowering locus T
9	176.8	20.7	668	AAZ28491	Flowering locus T

10	176	20.6	762	24	ABK82093	Novel floral meris
11	176	20.6	792	24	ABK82091	DNA encoding novel
12	176	20.6	792	24	ABK82092	DNA encoding novel
13	176	20.6	1225	24	ABK82122	DNA encoding novel
14	175	20.4	787	24	ABK82094	Novel floral meris
15	161.2	18.8	519	22	AAZ28491	Flowering locus T
16	145.8	17.0	4512	19	AAZ28491	Flowering locus T
17	116	13.6	929	18	AAZ28491	Flowering locus T
18	82.6	9.6	3696	22	AAZ28491	Flowering locus T
19	80	9.3	1430	18	AAZ28491	Flowering locus T
20	71.8	8.4	822	12	AAZ28491	Flowering locus T
21	63	7.4	4952	22	AAZ28491	Flowering locus T
22	55.6	6.5	567	24	ABK82094	Novel floral meris
23	52.8	6.2	2426	22	AAZ28491	Flowering locus T
24	51.8	6.1	1637	20	AAZ28491	Flowering locus T
25	51.2	6.0	970	24	ABK73995	Novel floral meris
26	51	6.0	988	24	ABK74181	Novel floral meris
27	50.2	5.9	557	22	AAZ28491	Flowering locus T
28	50.2	5.9	18585	24	ABK34609	Novel floral meris
29	50	5.8	649	22	AAZ28491	Flowering locus T
30	49.2	5.7	503	23	ABK41982	Novel floral meris
31	49.2	5.7	925	24	ABK74030	Novel floral meris
32	49.2	5.7	978	22	ABK7091	Novel floral meris
33	49.2	5.7	83391	24	ABK67094	Novel floral meris
34	49	5.7	1012	22	ABK7106	Novel floral meris
35	48.8	5.7	956	24	ABK74279	Novel floral meris
36	48.8	5.7	2637	24	ABK34120	Novel floral meris
37	48.6	5.7	427	24	ABK54500	Novel floral meris
38	48.6	5.7	475	22	AAZ28491	Flowering locus T
39	48.4	5.7	7589	24	ABK28390	Novel floral meris
40	48.2	5.6	367	22	AAZ28491	Flowering locus T
41	48.2	5.6	939	22	ABK74051	Novel floral meris
42	48	5.6	551	21	AAZ28491	Flowering locus T
43	48	5.6	654	22	AAZ28491	Flowering locus T
44	48	5.6	910	24	ABK73980	Novel floral meris
45	48	5.6	910	24	ABK73981	Novel floral meris

ALIGNMENTS

RESULT 1	AAZ28490	standard; cDNA; 856 BP.
ID	AAZ28490	
AC	AAZ28490	
XX		
DF	17-JAN-2000	(first entry)
XX		
DE	Flowering locus T (FT) gene.	
XX		
KW	Flowering locus T gene; FT; flowering time; modulator; early flowering;	
KW	antibody; cellular binding protein; crop; ss.	
XX		
OS	Arabidopsis thaliana.	
XX		
PH	Key	Location/Qualifiers
FT	CDS	63..590
FT		/*tag= a
FT		/product= FT
XX		/note= "Flowering Locus T"
XX		
XX	W09953070-A1.	
XX		
PD	21-OCT-1999.	
XX		
PF	13-APR-1999;	99MO-US08151.
XX		
PR	15-APR-1998;	98US-0060726.
XX		
PA	(SALK) SALK INST BIOLOGICAL STUDIES.	
XX		
PI	Weigel D;	

xx WPI: 1999-611305/52.
 DR P-PSDB: AAY49098.
 xx New flowering locus T polypeptide that regulates flowering time,
 PT particularly used to accelerate flowering -
 PS Claim 5; Fig 2; 64pp: English.
 CC This sequence is the flowering locus T (FT) gene of Arabidopsis thaliana.
 CC FT regulates flowering in plants by modulating flowering time.
 CC Overexpression of FT results in early flowering, while loss of function
 CC mutations or antisense directed to FT causes late flowering. The FT
 CC polypeptide has a molecular weight of approximately 20kd, and is located
 CC on chromosome 1. The FT polypeptide is used in the invention to modulate
 CC flowering time in many mono and di-cotyledonous plants. The FT
 CC polynucleotide sequence is used for recombinant production of the
 CC polypeptide, and as a source of antisense, ribozyme or triplex forming
 CC sequences. The FT polypeptide can also be used to raise antibodies and to
 CC screen for modulators or cellular binding proteins. The methods of the
 CC invention allow for the production of crops at any time of year.
 xx
 SO Sequence 856 BP; 263 A; 150 C; 194 G; 249 T; 0 other;

Query Match 100.0%; Score 856; DB 20; Length 856;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 Matches 856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY - 1 TCTAGAACTAGTATCCCGGGCTGCAGAAATTCAGACAGAGTTGTTCAAGATCAA 60
 Db 1 TCTAGAACTAGTATCCCGGGCTGCAGAAATTCAGACAGAGTTGTTCAAGATCAA 60
 QY 61 AGATGCTATTAATTAAGAGACCCCTTATAGTAAAGAGAGTTGGAGAGCTTCTTG 120
 Db 61 AGATGCTATTAATTAAGAGACCCCTTATAGTAAAGAGAGTTGGAGAGCTTCTTG 120
 QY 121 ATCGTTTAATAGATCACTCACTCAAGTTACTTATGCGCAAGAGAGGACTAATG 180
 Db 121 ATCGTTTAATAGATCACTCACTCAAGTTACTTATGCGCAAGAGAGGACTAATG 180
 QY 181 GCTTGATCTAAGGCTTCTCAGGTTCAAAACCAAGAGAGTTGATGGTGGAGAAG 240
 Db 181 GCTTGATCTAAGGCTTCTCAGGTTCAAAACCAAGAGAGTTGATGGTGGAGAAG 240
 QY 241 ACCTGAGAACTTCTATACCTTGTATGTGATGATCAAGATGTTCAAGTCCCTAGCAAC 300
 Db 241 ACCTGAGAACTTCTATACCTTGTATGTGATGATCAAGATGTTCAAGTCCCTAGCAAC 300
 QY 301 CTCACCTCCGAGAAATCTCATTTGTTGTTGATGATATCCCTCTACAACTGGAACAA 360
 Db 301 CTCACCTCCGAGAAATCTCATTTGTTGTTGATGATATCCCTCTACAACTGGAACAA 360
 QY 361 CTTTGGCAATGAGATTTGTGTAGCAAAATCCAAAGTCCCACTCAGAGAAATTCATCGTG 420
 Db 361 CTTTGGCAATGAGATTTGTGTAGCAAAATCCAAAGTCCCACTCAGAGAAATTCATCGTG 420
 QY 421 TCGTGTATTAATTTGTTGACAGCTTGGCAGCAAAAGTATGACACAGAGGTGGCCG 480
 Db 421 TCGTGTATTAATTTGTTGACAGCTTGGCAGCAAAAGTATGACACAGAGGTGGCCG 480
 QY 481 AGAATCTTAACACTGCGAGATTTGTGTAGATCTACATCTGAGGCTTCCCGTGGCCGAG 540
 Db 481 AGAATCTTAACACTGCGAGATTTGTGTAGATCTACATCTGAGGCTTCCCGTGGCCGAG 540
 QY 541 TTTTCTAATTTGTCAGAGGAGAGTGGCTGCGGAGAAAGATTTAGATGGCTTCTT 600
 Db 541 TTTTCTAATTTGTCAGAGGAGAGTGGCTGCGGAGAAAGATTTAGATGGCTTCTT 600
 QY 601 CTTTATTAACCAATTTGATATGATCTATGATGATTTATGATATTTTAA 660
 Db 601 CTTTATTAACCAATTTGATATGATCTATGATGATTTATGATATTTTAA 660
 QY 661 TTTAATAACCAATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720

Db 661 TTTAATAACCAATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 QY 721 TATAGTGTGTAATAAATGAGAGGAGGAGAAATGAGAGTGTACTATATATAGTG 780
 Db 721 TATAGTGTGTAATAAATGAGAGGAGGAGGAGAAATGAGAGTGTACTATATAGTG 780
 QY 781 TGTGATGCGAT 840
 Db 781 TGTGATGCGAT 840
 QY 841 AAAAAAAAAAATCTCGAG 856
 Db 841 AAAAAAAAAAATCTCGAG 856
 RESULT 2
 AAZ28491/c
 ID AAZ28491 standard; cDNA; 856 BP.
 AC AAZ28491;
 AC AAZ28491;
 DT 17-JAN-2000 (first entry)
 DE Flowering locus T (FT) gene antisense insert.
 DE Flowering locus T gene; FT; flowering time; modulator; early flowering;
 KW antibody; cellular binding protein; crop; antisense construct; ss.
 KW Arabidopsis thaliana.
 OS Arabidopsis thaliana.
 PN W09953070-AL.
 PD 21-OCT-1999.
 PE 13-APR-1999; 99WO-US08151.
 PF 15-APR-1998; 98US-0060726.
 PA (SALK) SALK INST BIOLOGICAL STUDIES.
 PI Weigel D;
 DR WPI: 1999-611305/52.
 XX New flowering locus T polypeptide that regulates flowering time,
 PT particularly used to accelerate flowering -
 PS Example 2; Fig 3; 64pp: English.
 CC This is the flowering locus T (FT) gene antisense polynucleotide
 CC sequence. This sequence is used in the production of the antisense
 CC construct of the invention psK1060. FT regulates flowering in plants by
 CC modulating flowering time. Overexpression of FT results in early
 CC flowering, while loss of function mutations or antisense directed to FT
 CC causes late flowering. The FT polypeptide has a molecular weight of
 CC approximately 20kd, and is located on chromosome 1. The FT polypeptide is
 CC used in the invention to modulate flowering time in many mono and
 CC di-cotyledonous plants. The FT polynucleotide sequence is used for
 CC recombinant production of the polypeptide, and as a source of antisense,
 CC ribozyme or triplex forming sequences. The FT polypeptide can also be
 CC used to raise antibodies and to screen for modulators or cellular binding
 CC proteins. The methods of the invention allow for the production of crops
 CC at any time of year.
 SO Sequence 856 BP; 249 A; 194 C; 150 G; 263 T; 0 other;
 Query Match 100.0%; Score 856; DB 20; Length 856;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 Matches 856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCTAGAACTAGTATCCCGGGCTGCAGAAATTCAGACAGAGTTGTTCAAGATCAA 60
 Db 1 TCTAGAACTAGTATCCCGGGCTGCAGAAATTCAGACAGAGTTGTTCAAGATCAA 60

Db 856 TCTAGACATGATGATCCCGGGGCTGCAGAAATTCAGACGAGGTTGTTCAAGATCAA 797
OY 61 AGATGCTAATAATTAAGACCTCTTATAGACAGAGTTGGAGAGTTCTTG 120
Db 796 AGATGCTAATAATTAAGACCTCTTATAGACAGAGTTGGAGAGTTCTTG 737
OY 121 ATCCGTTTAAATGATCAATCACTCTAAAGGTTACTTATGGCCAAAGAGAGTACTAATG 180
Db 736 ATCCGTTTAAATGATCAATCACTCTAAAGGTTACTTATGGCCAAAGAGAGTACTAATG 677
OY 181 GCTTGATCTAAGCCCTTCTCAGGTTCAAAACAGCCAGAGTTGATGTTGGAGAG 240
Db 676 GCTTGATCTAAGCCCTTCTCAGGTTCAAAACAGCCAGAGTTGATGTTGGAGAG 617
OY 241 ACCTGAGAACTCTTACTTGGTATGTTGATCCAGATGTTCCAAAGCCAGAAC 300
Db 616 ACCTGAGAACTCTTACTTGGTATGTTGATCCAGATGTTCCAAAGCCAGAAC 557
OY 301 CTCACCTCGAGAAATCTCCATTGGTGTGACTGATATCCCTGTACAACTGAGAACAA 360
Db 556 CTCACCTCGAGAAATCTCCATTGGTGTGACTGATATCCCTGTACAACTGAGAACAA 457
OY 361 CCTTGGCAATGAGATGTGTGTACGAAAATCCAAAGTCCCACTGCAAGATTCATCGTG 420
Db 496 CCTTGGCAATGAGATGTGTGTACGAAAATCCAAAGTCCCACTGCAAGATTCATCGTG 437
OY 421 TCGTGTATATGTTTCCACACCTTGGCAGGAAACAGTATGCAACCGGTTGGCGCC 480
Db 436 TCGTGTATATGTTTCCACACCTTGGCAGGAAACAGTATGCAACCGGTTGGCGCC 377
OY 481 AGAAGCTTCAACCTCGAGTTTGTGAGATCTACAAATCTCGGCTCCCGTGGCGCAG 540
Db 376 AGAAGCTTCAACCTCGAGTTTGTGAGATCTACAAATCTCGGCTCCCGTGGCGCAG 317
OY 541 TTTTCTCAATTTGTCAAGAGGAGAGTGCTGCGAGAGAGAACATTTAGATGGCTCTT 600
Db 316 TTTTCTCAATTTGTCAAGAGGAGAGTGCTGCGAGAGAGAACATTTAGATGGCTCTT 257
OY 601 CCTTAAACCATGATATGATCTGATCTGATGAGATTTAGATTAAGATTTTAA 660
Db 256 CCTTAAACCATGATATGATCTGATCTGATGAGATTTAGATTAAGATTTTAA 197
OY 661 TTTAATACCATTTTATGATAGAGTAACGAGTATGATCTTATAGTTCAATA 720
Db 196 TTTAATACCATTTTATGATAGAGTAACGAGTATGATCTTATAGTTCAATA 137
OY 721 TATTAAGTGTATTAATAATGAGAGGAGAGAAATGAGAGTGTACTTATATAGTG 780
Db 136 TATTAAGTGTATTAATAATGAGAGGAGAGAAATGAGAGTGTACTTATATAGTG 77
OY 781 TGTGATGCGATATTTATTTATCTACATGAATGAAGTGTATTTATAAAAAAAA 840
Db 76 TGTGATGCGATATTTATTTATCTACATGAATGAAGTGTATTTATAAAAAAAA 17
OY 841 AAAAAAAAAAAGTCGAG 856
Db 16 AAAAAAAAAAAGTCGAG 1

RESULT 3
AAC34682
ID AAC34682 standard; DNA; 775 BP.
XX AAC34682;
AC
AC 17-OCT-2000 (first entry)
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 7506.
XX
XX
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX

OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.

PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141844.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.

PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156596.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157153.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161993.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 80.9%; Score 692.4; DB 21; Length 775;
Best Local Similarity 99.9%; Pred. No. 5,3e-152;
Matches 693; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 45 GTTGTTCAGATCAAGATGCTATAATATAGAGACCCCTTATAGTAGAGAGCTT 104
|||||
DB 65 GTTGTTCAGATCAAGATGCTATAATATAGAGACCCCTTATAGTAGAGAGCTT 124
|||||
QY 105 GTTGAGACGTTCTTGATCCGTTTATATAGATCAATCACTCTTAAGGTTACTTATGGCCAA 164
|||||
DB 125 GTTGAGACGTTCTTGATCCGTTTATATAGATCAATCACTCTTAAGGTTACTTATGGCCAA 184
|||||
QY 165 AGAGAGGTGACTAATGGCTTGATAGGCTTCTAGGTTCAAAACAGCAAGAGCTT 224
|||||
DB 185 AGAGAGGTGACTAATGGCTTGATAGGCTTCTAGGTTCAAAACAGCAAGAGCTT 244
|||||
QY 225 GAGATTGGTGAGAGACCTCAGAACTCTATACTTTGGTTAGTGATCCAGATGTT 284
|||||
DB 245 GAGATTGGTGAGAGACCTCAGAACTCTATACTTTGGTTAGTGATCCAGATGTT 304
|||||
QY 285 CCAAGTCTAGCAACCCCTCAGCAATATCTCCATTGGTGGTACTGATATCCCT 344
|||||
DB 305 CCAAGTCTAGCAACCCCTCAGCAATATCTCCATTGGTGGTACTGATATCCCT 364
|||||
QY 345 GCTACAACTGGACAACTTTGGCAATGAGATTGTTGCAAAATCCAAAGTCCACT 404
|||||
DB 365 GCTACAACTGGACAACTTTGGCAATGAGATTGTTGCAAAATCCAAAGTCCACT 424
|||||
QY 405 GCAGGAATTCATCGTGTGTTTATATTTGTTGACAGCTTGCGAGCAACAGTGTAT 464
|||||

```
Db 425 GCAGGAATTCATGCTGTCGTTTATATGTTTCAGACAGCTGGAGCAACAGTGTAT 484
QY 465 GCACGAGGGTGGCGCCAGAACTTCAACACTCGGAGTTTCTAGATCTTCAATCTCGGC 524
Db 485 GCACCGAGGGTGGCGCCAGAACTTCAACACTCGGAGTTTCTAGATCTTCAATCTCGGC 544
QY 525 CTTCGCCGTGGCCGACAGTTTCTCAATTTGTCAGAGGAGAGTGGCCGAGGAGAGA 584
Db 545 CTTCGCCGTGGCCGACAGTTTCTCAATTTGTCAGAGGAGAGTGGCCGAGGAGAGA 604
QY 585 CTTTAGATGGCTTCTCTTATACCAATTGATTTGATCTGATGATGATTTATGC 644
Db 605 CTTTAGATGGCTTCTCTTATACCAATTGATTTGATCTGATGATGATTTATGC 664
QY 645 ATCTATAGTATTTTATTTATTAACATTTTATGATACGATACGACGAGGTGATGTC 704
Db 665 ATCTATAGTATTTTATTTATTAACATTTTATGATACGATACGACGAGTATGATGC 724
QY 705 CTATAGTATTCATATATATAGTGTATATATAA 738
Db 725 CTATAGTATTCATATATATAGTGTATATATAA 758

RESULT 4
AAC48359
ID AAC48359 standard; DNA; 754 BP.
XX
AC AAC48359;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 57192.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway;
XX metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-72.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000BP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130649.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130691.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.

PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137228.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139819.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145087.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
```

PR	8-JUL-1999;	9905-0145951;
PR	02-AUG-1999;	9905-0145388;
PR	02-AUG-1999;	9905-0145386;
PR	02-AUG-1999;	9905-0145387;
PR	03-AUG-1999;	9905-0147038;
PR	04-AUG-1999;	9905-0147204;
PR	04-AUG-1999;	9905-0147302;
PR	05-AUG-1999;	9905-0147192;
PR	05-AUG-1999;	9905-0147260;
PR	05-AUG-1999;	9905-0147303;
PR	06-AUG-1999;	9905-0147416;
PR	09-AUG-1999;	9905-0147493;
PR	10-AUG-1999;	9905-0147935;
PR	11-AUG-1999;	9905-0148171;
PR	12-AUG-1999;	9905-0148351;
PR	13-AUG-1999;	9905-0148565;
PR	13-AUG-1999;	9905-0148684;
PR	16-AUG-1999;	9905-0145368;
PR	17-AUG-1999;	9905-0145375;
PR	18-AUG-1999;	9905-0145915;
PR	20-AUG-1999;	9905-0149426;
PR	20-AUG-1999;	9905-0149722;
PR	20-AUG-1999;	9905-0149723;
PR	20-AUG-1999;	9905-0149929;
PR	23-AUG-1999;	9905-0145902;
PR	23-AUG-1999;	9905-0145930;
PR	25-AUG-1999;	9905-0150566;
PR	26-AUG-1999;	9905-0150884;
PR	27-AUG-1999;	9905-0151065;
PR	27-AUG-1999;	9905-0151066;
PR	30-AUG-1999;	9905-0151303;
PR	31-AUG-1999;	9905-0151438;
PR	01-SEP-1999;	9905-0151930;
PR	07-SEP-1999;	9905-0153363;
PR	10-SEP-1999;	9905-0153707;
PR	13-SEP-1999;	9905-0153758;
PR	15-SEP-1999;	9905-0154019;
PR	16-SEP-1999;	9905-0154038;
PR	20-SEP-1999;	9905-0154779;
PR	22-SEP-1999;	9905-0155139;
PR	23-SEP-1999;	9905-0155486;
PR	24-SEP-1999;	9905-0155659;
PR	28-SEP-1999;	9905-0155458;
PR	29-SEP-1999;	9905-0155596;
PR	04-OCT-1999;	9905-0157117;
PR	05-OCT-1999;	9905-0157753;
PR	06-OCT-1999;	9905-0157855;
PR	07-OCT-1999;	9905-0158025;
PR	08-OCT-1999;	9905-0158332;
PR	12-OCT-1999;	9905-0158369;
PR	13-OCT-1999;	9905-0159293;
PR	13-OCT-1999;	9905-0159294;
PR	13-OCT-1999;	9905-0159325;
PR	14-OCT-1999;	9905-0159330;
PR	14-OCT-1999;	9905-0159331;
PR	14-OCT-1999;	9905-0159537;
PR	14-OCT-1999;	9905-0159568;
PR	18-OCT-1999;	9905-0159584;
PR	21-OCT-1999;	9905-0160741;
PR	21-OCT-1999;	9905-0160767;
PR	21-OCT-1999;	9905-0160768;
PR	21-OCT-1999;	9905-0160770;
PR	21-OCT-1999;	9905-0160814;
PR	21-OCT-1999;	9905-0160815;
PR	22-OCT-1999;	9905-0160980;
PR	22-OCT-1999;	9905-0160981;
PR	22-OCT-1999;	9905-0161009;
PR	25-OCT-1999;	9905-0161404;
PR	25-OCT-1999;	9905-0161405;
PR	26-OCT-1999;	9905-0161436;
PR	26-OCT-1999;	9905-0161659;

PR	26-OCT-1999;	99US-0161360
PR	26-OCT-1999;	99US-0161361
PR	28-OCT-1999;	99US-0161920
PR	28-OCT-1999;	99US-0161992
PR	28-OCT-1999;	99US-0161993
PR	29-OCT-1999;	99US-0162142

Query Match	80.8%	Score 692	DB 21	Length 754
Best Local Similarity	100.0%	Pred. No. 6.5e-152		
Matches 692	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Oy	45	GTTCGTTCAAGATCAAAATGCTATATAATTAAGAGACCCCTTATAGTAAGCAGAGTT	104
Db	63	GTTTGTTCAAAGTTCAAAGATGTCATATAATTAAGAGACCCCTTATAGTAAGCAGAGTT	122
Oy	105	GTTGAGACGTTCTTGATCCGTTTAATATGATCAATCACTCTAAAGGTTACTTATGGCCAA	164
Db	123	GTTGGAGACGTTCTTGATCCGTTTAATATGATCAATCACTCTAAAGGTTACTTATGGCCAA	182
Oy	165	AGAGAGGTGACTAATGGCTTGGATCTAAGGCCCTTCAGGTTCAAAACAGCCAAAGTT	222
Db	183	AGAGAGGTGACTAATGGCTTGGATCTAAGGCCCTTCAGGTTCAAAACAGCCAAAGTT	242
Oy	225	GAGATGGTGGAGAAAGACCTCAGGAACCTCTATACCTTGGTATGGTGATCCAGATGTT	284
Db	243	GAGATGGTGGAGAAAGACCTCAGGAACCTCTATACCTTGGTATGGTGATCCAGATGTT	302
Oy	285	CCAAAGTCTAGCAACCCCTCACCTCCGAGAAATATCTCCATTGGTGGTGACTATATCCCT	344
Db	303	CCAAAGTCTAGCAACCCCTCACCTCCGAGAAATATCTCCATTGGTGGTGACTATATCCCT	362
Oy	345	GCTACAACTGGAAACAACCTTGGAAAGATGTGGTGTACGAAATCCAAAGTCCACT	404
Db	363	GCTACAACTGGAAACAACCTTGGAAAGATGTGGTGTACGAAATCCAAAGTCCACT	422
Oy	405	GCAGAAATTCATCGTGTCTGTATATATTGTTGCAGACGTGGCAGGCAAAACAGTGTAT	464
Db	423	GCAGAAATTCATCGTGTCTGTATATATTGTTGCAGACGTGGCAGGCAAAACAGTGTAT	482
Oy	465	GCACCAGGCTGGCGCCAGACCTTCAACACCTGCGAGATTGCTGAGATCTACATCTCGGC	522
Db	483	GCACCAGGCTGGCGCCAGAACTTCAACACCTGCGAGATTGCTGAGATCTACAAATCTCGGC	542
Oy	525	CTTCCCGGCGCCAGATTTCTCAAAATGTGCAGAGGAGAGATGGCTCGCGAGGAAGAGA	584
Db	543	CTTCCCGGCGCCAGATTTCTTACAAATGTGCAGAGGAGAGATGGCTCGCGAGGAAGAGA	602
Oy	585	CTTTAGATGCGCTCTCTCTTATTAACCAATTGATATTGCATACCTGATGAGATTTATGC	644
Db	603	CTTTAGATGCGCTCTCTCTTATTAACCAATTGATATTGCATACCTGATGAGATTTATGC	662
Oy	645	ATCTATAGTATTTTATTTATTAACCATTTTATATGATACGAGTAACGAAGCGTGATGATGC	704
Db	663	ATCTATAGTATTTTATTTTATTAACCATTTTATATGATACGAGTAACGAAGCGTGATGATGC	722
Oy	705	CTATAGTATGTCATATATTAAGTGTGAATATA 736	
Db	723	CTATAGTATGTCATATATTAAGTGTGAATATA 754	
RESULT 5			
AAA60683			
ID	AAA60683 standard; DNA: 528 BP.		
XX	AAA60683:		
AC			
XX			
DT	26-OCT-2000 (first entry)		
XX			
DE	Arabidopsis thaliana nucleotide sequence SEQ ID NO:2.		
XX			
XX	Arabidopsis thaliana; Cruciferae; plant; control; flowering;		
KM	solar radiation; ds.		
XX			

OS Arabidopsis thaliana.
XX JP2000139250-A.
XX 23-MAY-2000.
XX 11-NOV-1998; 98JP-0320219.
XX 11-NOV-1998; 98JP-0320219.
XX (TORA) TORAY IND INC.
XX WPI; 2000-425906/37.
XX P-PSDB; AAB12459.
XX
PT A method to accelerate plant generation and generation accelerated
PT plants -
XX
XX Claim 5; Page 5; 6pp; Japanese.
XX
CC the present invention describes a method to accelerate plant generation
CC and generation accelerated plants. The method uses a controlling gene
CC functioning in the downstream of a gene under the control of solar
CC radiation to accelerate plant generation using a gene functioning to
CC accelerate the flowering time regardless of solar radiation. The method
CC can control flowering time to a desired period by shortening the
CC juvenile stage. The present sequence represents a specifically claimed
CC Arabidopsis nucleotide sequence, which is used in the exemplification
CC of the present invention.
XX
SQ Sequence 528 BP; 143 A; 111 C; 129 G; 145 T; 0 other;

Query Match 61.7%; Score 528; DB 21; Length 528;
Best Local Similarity 100.0%; Pred. No. 1.1e-113;
Matches 528; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 ATGCTATTAATTAATAGAGCCCTCTTATAGTACAGAGTTGTTGAGAGCTTCTGAT 122
DB 1 ATGCTATTAATTAATAGAGCCCTCTTATAGTACAGAGTTGTTGAGAGCTTCTGAT 60
QY 123 CCGTTTAATAGATCAATCACTCTTAAAGTTACTTATGCGCAAGAGAGTCAATAGGC 182
DB 61 CCGTTTAATAGATCAATCACTCTTAAAGTTACTTATGCGCAAGAGAGTCAATAGGC 120
QY 183 TTGATCTAAGCCCTTCACAGTTCAAAACAAGCAAGTTGAGATTGGTGAAGAAGC 242
DB 121 TTGATCTAAGCCCTTCACAGTTCAAAACAAGCAAGTTGAGATTGGTGAAGAAGC 180
QY 243 CTCAGGAACCTCTACTTGTGTTATGGTGCAGATGTTCCAAAGTCCCTAGCAACCT 302
DB 181 CTCAGGAACCTCTACTTGTGTTATGGTGCAGATGTTCCAAAGTCCCTAGCAACCT 240
QY 303 CACCTCCGAGATATCTCCATTTGTTGGTGAATATCCCTGCTACCACTGGAACAAC 362
DB 241 CACCTCCGAGATATCTCCATTTGTTGGTGAATATCCCTGCTACCACTGGAACAAC 300
QY 363 TTGAGCAATGAGATTGTGTGTTACGAAATCCCAAGTCCCACTGAGGAATTCATGTC 422
DB 301 TTGAGCAATGAGATTGTGTGTTACGAAATCCCAAGTCCCACTGAGGAATTCATGTC 360
QY 423 GTGTTTATATGTTTCGACAGTTTGGCAGGCAAAAGTGTATGACACAGAGTGGCCGAG 482
DB 361 GTGTTTATATGTTTCGACAGTTTGGCAGGCAAAAGTGTATGACACAGAGTGGCCGAG 420
QY 483 AACTTCAACACTCGCGAGTTTGTGAGATCTCAATCTCGGCTTCCGTCGCCAGTT 542
DB 421 AACTTCAACACTCGCGAGTTTGTGAGATCTCAATCTCGGCTTCCGTCGCCAGTT 480
QY 543 TTCTCAATTTGTGAGAGGAGAGTGGCTGCGGAGGAAGAAGACTTTAG 590
DB 481 TTCTCAATTTGTGAGAGGAGAGTGGCTGCGGAGGAAGAAGACTTTAG 528

RESULT 6
ID AAC42966
XX AAC42966 standard; DNA; 528 BP.
AC
XX AAC42966;
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 37529.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 18-MAY-1999; 99US-0134370.
PR 19-MAY-1999; 99US-0134768.
PR 20-MAY-1999; 99US-0134941.
PR 21-MAY-1999; 99US-0135124.
PR 24-MAY-1999; 99US-0135353.
PR 25-MAY-1999; 99US-0135629.
PR 27-MAY-1999; 99US-0136021.
PR 28-MAY-1999; 99US-0136392.
PR 01-JUN-1999; 99US-0136782.
PR 03-JUN-1999; 99US-0137222.
PR 04-JUN-1999; 99US-0137528.
PR 07-JUN-1999; 99US-0137502.
PR 08-JUN-1999; 99US-0137724.
PR 10-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 14-JUN-1999; 99US-0138847.
PR 16-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 17-JUN-1999; 99US-0139453.
PR 18-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.

PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140891.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 02-JUL-1999; 99US-0142154.
PR 06-JUL-1999; 99US-0142055.
PR 08-JUL-1999; 99US-0142390.
PR 09-JUL-1999; 99US-0142803.
PR 12-JUL-1999; 99US-0142820.
PR 13-JUL-1999; 99US-0142877.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 21-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147204.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.

PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152263.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160981.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 44.1%; Score 377.6; DB 21; Length 528;
Best Local Similarity 82.2%; Pred. No. 1.2e-78;
Matches 434; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

OY 63 ATGCTATAAATATAGACCCCTTTATATAGCAGAGTGTGGAGACGTTCTTGAT 122
DB 1 ATGCTTTAAGTCGTAGAGATCCTTGTGTCGCGAGTGTGGAGATGTTCTTGAT 60
OY 123 CCGTTAATAGATCAATCACTCTAAGGTTACTTATGCCCAAGAGAGGTGCTAATGCC 182
DB 61 CCTTTCACGAGGTGTGCTCTTAAGTCACTTATGGCCATAGAGAGGTGCTAATGCC 120
OY 183 TTGATCTAAGGCTTCTAGGTTCTTAAGCAAGCCAGAGTGTGAGTGTGGAGAGAC 242
DB 121 TTGATCTAAGGCTTCTTAAGTGTGAGCAACCAATAGTGTGAGATGTGGAGAGAC 180

OY	243	CTCAGGAACCTCTTACTGTTGGTATGATGGGATATCCAAATCTTCCAACTCTACCAACCT	302
Db	181	TTTCGAAATTTCTACACCTGGTGTATGGTGAATCCAAATGTGCCGAATCCAAACACCTT	240
OY	303	CACCTCCGAGAAATATCTCCATATGGTGGTGACTATATCCCTGCTACCAATCGGAACAAC	352
Db	241	CACCAACGAGAAATCTCCACATGGTGTGGTACTATATTACTGCAACCACTGGAAATGCC	300
OY	363	TTTGGCAATGAGATTGTGTGTTACGAAATATCCAGTCCCACTGCAGGAATTCATCTGTTC	422
Db	301	TTTGGCAATGAGGTGGTGTGCTACGAGAGTCCACAGTCCCTCCGGGAAATTCATCTGATT	360
OY	423	GTGTTTATATTGTTTCGACAGCTTGCAGGCAACACAGTATGTCACCAGGGTGGCCGAC	482
Db	361	GTGTTGGTATGTTCCGGCACTCGGAAGCAAAACGGTTATATGACCGGGGGTGGCCAA	420
OY	483	AACTTCAACACTCGCCGAGTTTGTCTGAATATCTACATCTCGGCTTCCCGTGGCCGAGTT	542
Db	421	CAGTTCAACACTCGTGGATTTGGTCGAATCTACATATTGGTCTTCTCTGTGGCTGCCTT	480
OY	543	TTTACACATTGTCAGAGGGAGTGGGTGGCGGAGAGAAAGACTTTTG	590
Db	481	TACTTCAACTGCCAGAGGGAGAAATGGCTGTGGGGGAGAAAGACGTG	528

```

RESULT 7
AAA60684
ID AAA60684 standard; DNA; 528 BP.
XX
XX AAA60684;
AC
XX
XX 26-OCR-2000 (first entry)
XX
XX Arabidopsis thaliana nucleotide sequence SEQ ID NO:3.
DE
XX Arabidopsis thaliana; Cruciferae; plant; control; flowering;
XX Arabidopsis thaliana; ds.
XX
XX Arabidopsis thaliana.
OS
XX Arabidopsis thaliana.
XX
XX JP2000139250-A.
XX
XX
XX 23-MAY-2000.
XX
XX 11-NOV-1998; 98JP-0320219.
XX
XX 11-NOV-1998; 98JP-0320219.
XX
XX (TORA ) TORAY IND INC.
XX
XX
XX WPI; 2000-425906/37.
XX
XX
XX A method to accelerate plant generation and generation accelerated
XX plants -
XX
XX
XX PS Claim 5; Page 5; 6pp; Japanese.
XX
XX
XX the present invention describes a method to accelerate plant generation
XX and generation accelerated plants. The method uses a controlling gene
XX functioning in the downstream of a gene under the control of solar
XX radiation to accelerate plant generation using a gene functioning to
XX accelerate the flowering time regardless of solar radiation. The method
XX can control flowering time to a desired period by shortening the
XX juvenile stage. The present sequence represents a specifically claimed
XX Arabidopsis nucleotide sequence, which is used in the exemplification
XX of the present invention.
XX
XX
SQ Sequence 528 BP; 122 A; 117 C; 142 G; 147 T; 0 other;

Query Match 43.7%; Score 374.4; DB 21; Length 528;
Best Local Similarity 81.8%; Pred. NO. 6.9e-78;
Matches 432; Conservative 0; Mismatches 96; Indels 0; Gaps

```

Qy	63	ANGTCATATAAATATTAAGAGACCCTCTATATAGTAAAGCAAGATTGTGTGAAGACGTCCTTGAT	122
Db	1	ATGCTTTTAAAGTCGTAGAGATCTCTCTGTGTGGCGAGCTGTGTGGAGATGTTCTTTGAT	60
Qy	123	CCGTTTAATATGATCAATCACTCTTAAGGTATCTATATAGTACCAAGAAGAGAGGTACATAATGCG	182
Db	61	CGTTTCACGAGGTGGTCTCTCTTAAGTCACTTATATGCCATATAGAGAGGTTACTAATGCC	120
Qy	183	TTTGATCTTAAGCCCTTCTCAAGTTCAAAACAGCCAAAGATTGAGTTGGTGGAGAAGAC	242
Db	121	TTGGATCTAAGCCCTCTCAAGTTCTGAACAAACATATAGTGGAGATTTGAGAGAGAGAC	180
Qy	243	CTCAGGAATCTTAATCTTGTGTTATGATGGTGAATCAGATGTTCCAACTCTTACCAACCT	302
Db	181	TTTCAAAATTTCTACACTTGTTATGTTATGATGATCTGATGTGGCCGAGTCCAAACACCT	240
Qy	303	CACCTCCGAGATATCTTCATTTGTTGGTGAATATATCCCTGCTACAACTGGACAAACC	362
Db	241	CACCAACGAGATATCTTCACCTGCTGTGATGATCTATATACCTGGCAACATGGAAATGCC	300
Qy	363	TTTGGCAATGAGATTGTGTGTTAGGAATAATCCAACTGCCACTGGAGAAATTCATCGTGC	422
Db	301	TTTGGCAATGAGTGTGTGTGTCTACGACAGTCCACGTCCTCCCTGGGAATTCATCGTAT	360
Qy	423	GTGTTATATATGTTTGCACACTTGGCAGGCAACAACTGATATGCACAGGGGTGGCGCAG	482
Db	361	GTGTTGTGATTTGTTCCGCGCACTGGGAACAAACGCTTATATGCAACCGGGGTGGCGCA	420
Qy	483	AACTTCAACACTCGCGAGTTGCTGAAGTCTCAATCTCGGCTTCCCTGGCGCGCAGTT	542
Db	421	CAGTTCAACACTCGTGAATTTGCTGAATCTCAATCTTGGTCTTCTCTGTGGCTGCCTT	480
Qy	543	TTTCAACAATTTGTCAGAGGAGAGTGGCTGGCGAGAGAGCACTTNG	590
Db	481	TACTTCAACTCCAGAGGAGAAATGGCTGTGGGGGAGAGAAACGTNG	528

XX	RESULT 8
XX	AAC90636
ID	AAC90636 standard; cDNA; 522 BP.
XX	
XX	AAC90636;
XX	
DT	20-MAR-2001 (first entry)
XX	
DE	Strawberry flowering regulation protein coding sequence SEQ ID NO: 5.
XX	
KW	Strawberry; flowering regulation; floral homeotic gene; field crop;
KW	harvesting; fruit production; ss.
XX	
OS	Fragaria vesca.
XX	
PN	WO200071722-A1.
XX	
PD	30-NOV-2000.
XX	
PE	24-MAY-2000; 2000WO-US14297.
XX	
PR	25-MAY-1999; 99US-0318789.
PR	24-MAY-2000; 2000US-0318789.
XX	
PA	(DNAP) DNA PLANT TECHNOLOGY CORP.
XX	
PI	Oeller P, Gutterson N;
XX	
DR	WPI; 2001-025165/03.
DR	P-PSDB; AAB50266.
XX	
PT	Novel nucleic acid involved in controlling plant flowering processes
PT	useful for generating transgenic plants, in particular strawberry
PT	plants having altered flowering behavior such as early, delayed or
PT	day-neutral flowering
XX	

Db 392 TTGGTGTGTTCTGTGTACGGCAGAACGAAGCGTTATCTTTCCTAATTCCTCCG 441
||||| |||| | |||
Oy 477 GCGCAGAACTTCACAACCTGCAGAGTTTGCTGAGATCTACAACTCGGCCCTCCGCGCC 536
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 442 AGAGATCACTCATCAACACTCGTAATAATTGGGGTCGAGTAGATCTGTGGTCCGTCGCG 501
442 AGAGATCACTCATCAACACTCGTAATAATTGGGGTCGAGTAGATCTGTGGTCCGTCGCG 501
Oy 537 GCAGTTTTCTACAAATTGTTCAGAGGGAGA 564
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 502 GCCGCTCTCTTTAAACGACCAAGAGAAA 529
GCCGCTCTCTTTAAACGACCAAGAGAAA 529

RESULT 10
ABR82093
ID ABR82093 standard; cDNA; 762 BP.
XX AC
XX ABR82093;
DT 27-AUG-2002 (first entry)
XX DE
XX Novel floral meristem identity gene IpcENA contig #2.
KW Ryegrass; fescue; MAD5-box; MAD5; MAD5-like protein; CENTRORADIALIS;
KN CEN-1-like protein; APERLA2; AP2; AP2-like protein; HB;
HW Homeo-box protein; HB-like protein; plant growth; plant architecture;
RV Inflorescence development; flower development; embryo development;
KW seed development; flower organ identity; phase change; male sterility;
KV hybrid seed production; herbage quality; early maturing crop;
KW biomass increase; branching increase; blocking flowering;
KV allergenic pollen; floral meristem identity protein; ss.
XX
XX Lolium perenne.
OS
PN WO200233091-A1.
XX
PD 25-APR-2002.
XX
XX 17-OCT-2001; 2001WO-AU01311.
XX PF
XX 19-OCT-2000; 2000AU-0000873.
PR FR
XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRESEARCH LTD.
XX
PA Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
PI MPI, 2002-452388/48.
XX DR
XX
PT New substantially purified or isolated polypeptide e.g., MAD5-box,
PT CENTRORADIALIS, APERLA2, Homeo-box proteins, isolated from rye-grass or
PT fescue species, useful for controlling plant life cycles and/or growth
PT phases -
XX
XX Claim 4; Fig 32; 290pp; English.

The invention describes a substantially purified or isolated polypeptide (I) from a ryegrass (*Lolium* sp.) or fescue (*Festuca* sp.) species, such as MAD5-box (MADS) and MAD5-like proteins, CENTRORADIALIS (CEN) and CEN-1-like proteins, APERLA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB) and HB-like proteins, or their functionally active fragments or variants. Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a vector (IV) comprising (II), is useful for modifying plant life cycles and/or growth phases, flowering processes, flowering and/or plant architecture and/or flower and/or inflorescence development in a plant, which involves introducing (II), (III) or (IV) into the plant. The individual or simultaneous enhancement or downregulation of MAD5-box gene activities may alter flower, embryo and seed development, e.g., enhance or inhibit embryoid differentiation and growth or alter flower organ identity through conversion of one floral organ in another. Manipulation of CEN or HB activity in plants alters the control of phase change, flowering time and the number of leaves made before flowering. Manipulation of AP2 activity in plants alters flower organ identity through conversion of one floral organ in another, leads to a change in

Query Match	20.6%	Score 176;	DB 24;	Length 762;
Best Local Similarity	60.0%	Pred. No. 1.4e-31;		
Matches 312;	Conservative	0;	Mismatches 205;	Indels 3; Gaps 1
CC	the number of floral organs and flowering architecture. Manipulation of			
CC	flowering plant architecture has a wide range of applications such as:			
CC	inducing male sterility for hybrid seed production; changing flower			
CC	architecture for enhancing value of ornamentals; delaying flowering in			
CC	forage grasses thus stopping the formation of less digestible stems and			
CC	increasing herbage quality; altering flowering time allowing early			
CC	maturing crops; delaying vegetative phase to increase biomass production;			
CC	increasing branching to enhanced business in fruit trees; altering plant			
CC	size e.g. shorter plant stature; and in blocking flowering and reducing			
CC	release for allergenic pollen. This sequence represents a contig			
CC	polynucleotide novel floral meristem identity protein involved in floral			
CC	development and a potential target for manipulating plant life cycles.			
XX				
SO	Sequence 762 BP; 188 A; 178 C; 176 G; 220 T; 0 other;			
QY	81. GACCCTCTATATGTAAGCAGACTGTTGGAGACGCTTCGTGATCCGTTAATAGATCAATC 140			
DB	103 GAGCCTCTATATGTTGGTGTCTCATTTGGAGAAATCTGCATTCATTAAACCATCTGTG 162			
QY	141 ACTCTAAGGTTACTTATGSCCAAGAGAGGTGAC---TAATGCGTTGGATCTTAAGCCCT 197			
DB	163 AAGATGGTAGCAACCTATATACCTCAACAACAGCTGGTCTTCAATGTCATAGCTCTAACCA 222			
QY	198 TCTCAGGCTTCAAAACACAGCCAGAGTGTAGATTGGTGGAGAAAGCCTCAGAACTCTAT 257			
DB	223 TCAGCAGTTGTATCTTAACCAAGAGTAGAGGTTCAAGGGGGGTGACTGGCATCTTATTC 282			
QY	258 ACTTTGGTTATGGTGCATCCAGATGTTCCAAAGTCTTAGCAACCTCCACTCCGAGAATAT 317			
DB	283 ACATTTGTTATGGCGGACCCAGATGTCGACAGCAAGTATGCCATCTGCGGGAGACAT 342			
QY	318 CTCACATTGGTGTGATCTATATCCTGCTACAACTGGAACAACCTTTGGCAATGAGATT 377			
DB	343 CTTCACTGATTTGTCAGTATATACCTGGGACAAACAGATGCTTCAATTTGGGGGGAGGTC 402			
QY	378 GTGTGTTAGGAANAATCCCAAGTCCCACTGGAGAAATCATGTCGTGTTATATATGTTT 437			
DB	403 ATGAGCTATAGAGAGCCCAAGCCCAACATTTGGATTCACAGGTTCAATTTTGTGCTTTC 462			
QY	438 CGACAGCTTGGCAGGCAAAACAGTGTATGACCAAGAGGTGGCGCCAGAACTTCAACACTCGC 497			
DB	463 AAGCAGAAACGGAAGGACAGACTGATCTGTGCTTCTCTTCCAGGAGATCATTTCAACACCCG 522			
QY	498 GAGTTTGCTGAATCTCAATCTCGGCCCTTCCGCTGGCCGACGTTTCTCAACAATTTGAC 557			
DB	523 CAGTTTGCTGTGTATATATATCTTGGCCCTCCCTGTGGCTGTCTTACTTCATTTGTCAG 582			
QY	558 AGGAGAGTGGCTGCGGAGAGAAACACTTTTATGATGGCTT 597			
DB	583 AGAGAGACTGCTGCCAGAGAGCGGCTTAATAATGAGTTCTT 622			
RESULT 11				
ID	ABK82091			
AC	ABK82091 standard; cDNA; 792 BP.			
XX	ABK82091;			
DT	27-AUG-2002 (first entry)			
XX				
DE	DNA encoding novel floral meristem identity protein lpcena.			
XX				
KM	Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS;			
KM	CEN; CEN-like protein; APETALA2; AP2; AP2-like protein; HB;			
KM	Homeo-box protein; HB-like protein; plant growth; plant architecture;			
KM	inflorescence development; flower development; embryo development;			
KM	seed development; flower organ identity; phase change; male sterility;			
KM	hybrid seed production; herbage quality; early maturing crop;			
KM	biomass increase; branching increase; blocking flowering;			

KM allergenic pollen; floral meristem identity protein; gene: ss.
 OS Lolium perenne.
 PN WO200233091-A1.
 XX 25-APR-2002.
 PD 17-OCT-2001; 2001WO-AU01311.
 XX 19-OCT-2000; 2000AU-0000873.
 PR (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 XX Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
 PI WPI: 2002-452388/48.
 DR P-PSDB: ABG60933.
 XX
 DR New substantially purified or isolated polypeptide e.g., MADS-box,
 PT CENTRORADIALIS, APTAL2, Homeo-box proteins, isolated from ryegrass or
 PT fescue species, useful for controlling plant life cycles and/or growth
 PT phases
 XX
 PS Claim 4: Fig 30; 290pp; English.
 XX
 CC The invention describes a substantially purified or isolated polypeptide
 CC (I) from a ryegrass (Lolium sp.) or fescue (Festuca sp.) species, such as
 CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
 CC proteins, APTAL2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
 CC and HB-like proteins, or their functionally active fragments or variants.
 CC Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a
 CC vector (IV) comprising (II), is useful for modifying plant life cycles
 CC and/or growth phases, flowering processes, flowering and/or plant
 CC architecture and/or flower and/or inflorescence development in a plant,
 CC which involves introducing (II), (III) or (IV) into the plant. The
 CC individual or simultaneous enhancement or downregulation of MADS-box
 CC gene activities may alter flower, embryo and seed development, e.g.,
 CC enhance or inhibit embryo differentiation and growth or alter flower
 CC organ identity through conversion of one floral organ in another.
 CC Manipulation of CEN or HB activity in plants alters the control of phase
 CC change, flowering time and the number of leaves made before flowering.
 CC Manipulation of AP2 activity in plants alters flower organ identity
 CC through conversion of one floral organ in another, leads to a change in
 CC the number of floral organs and flowering architecture. Manipulation of
 CC flowering plant architecture has a wide range of applications such as:
 CC inducing male sterility for hybrid seed production; changing flower
 CC architecture for enhancing value of ornamentals; delaying flowering in
 CC forage grasses thus stopping the formation of less digestible stems and
 CC increasing herbage quality; altering flowering time allowing early
 CC maturing crops; delaying vegetative phase to increase biomass production;
 CC increasing branching to enhanced business in fruit trees; altering plant
 CC size e.g. shorter plant stature; and in blocking flowering and reducing
 CC release for allergenic pollen. This sequence encodes a novel floral
 CC meristem identity protein involved in floral development and a potential
 CC target for manipulating plant life cycles.
 XX
 XX Sequence 792 BP; 196 A; 181 C; 181 G; 232 T; 2 other;
 SQ
 Query Match 20.6%; Score 176; DB 24; Length 792;
 Best Local Similarity 60.0%; Pred. No. 1.4e-31;
 Matches 312; Conservative 0; Mismatches 205; Indels 3; Gaps 1;

DB 226 TCAGCAGTTGATCTAAACCAAGTAGAGTTACAGGGGGGTGACTTGGATCCTTATTC 285
 OY 258 ACTTTGTTATGGTGGATGCAGATGTTCCAAAGCTAGCAACCCCTACCTCGAGAAATAT 317
 DB 286 ACATTGTTATGGCGGAGCCCAAGATGTGCCAGGACCAAGTATCGTATCGCGGAGCAT 345
 OY 318 CTCATTTGTTGTTGCTGACTGATATCCCTGCTACAACTGGAACAACCTTGGCAATGAT 377
 DB 346 CTTCAGCTGATTTGCTAGTATATACCTGGGCAACAGATGCTTCATTTGGGGGAGTTC 405
 OY 378 GTGTGTAGAAAATCCAAAGTCCCACTGCAGGAATTCATGCTGTCTTATATGTTT 437
 DB 406 ATGAGCTATGAGAGCCCAAGCCCAATTCACCAAGTTCACATTTTGTGCTTTC 465
 OY 438 CGACAGCTTGGCGCAACAGTGTATGACACGAGGTGGCGCCAGCACTTCAACACTGCG 497
 DB 466 MAGCAGAACGGAAGGACGACTGATCTGTGCTTCTTACAGGATATTTCAACACCCCG 525
 OY 498 GAGTTTCTGAGATCTACATCTCGCTCCGCTGGCCGCAAGTTTCTACAAATGTCAG 557
 DB 526 CAGTTTGTGTTGATATGATCTTGGCTCCGCTGCTGCTGCTTACTTCAATGTCAG 585
 OY 558 AGGAGAGTGTGCTGCGGAGGAGACACTTTCATGCTT 597
 DB 586 AGAGAGACTGCTGCCAGAGGCGCTGAAATGAGTTCTT 625
 RESULT 12
 ABR82092
 ID ABR82092 standard; cDNA: 792 BP.
 XX
 AC ABR82092;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Novel floral meristem identity gene LpCENa contig #1.
 XX
 XX Ryegrass: fescue; MADS-box; MADS: MADS-like protein; CENTRORADIALIS;
 KW CEN: CEN-like protein; APTAL2; AP2; AP2-like protein; HB;
 KW Homeo-box protein; HB-like protein; plant growth; plant architecture;
 KW inflorescence development; flower development; embryo development;
 KW hybrid seed production; flower organ identity; phase change; male sterility;
 KW biomass increase; branching increase; blocking flowering;
 KW allergenic pollen; floral meristem identity protein; ss.
 XX
 OS Lolium perenne.
 XX
 PN WO200233091-A1.
 XX
 PD 25-APR-2002.
 XX
 PF 17-OCT-2001; 2001WO-AU01311.
 XX
 PR 19-OCT-2000; 2000AU-0000873.
 XX
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 XX
 XX Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
 PI WPI: 2002-452388/48.
 DR
 XX
 DR New substantially purified or isolated polypeptide e.g., MADS-box,
 PT CENTRORADIALIS, APTAL2, Homeo-box proteins, isolated from ryegrass or
 PT fescue species, useful for controlling plant life cycles and/or growth
 PT phases
 XX
 PS Claim 4: Fig 32; 290pp; English.
 XX
 CC The invention describes a substantially purified or isolated polypeptide
 CC (I) from a ryegrass (Lolium sp.) or fescue (Festuca sp.) species, such as

Db 406 ATGAGTATGAGACCCCAACCAATTCAGATTCATTTTGTGCTTC 465
QY 438 CGAAGCTTGGCAGCAACAGTGTATGCACAGGTTGGCCCAACTTAACACTGC 497
Db 466 AAGGANAAGCGAAGGACGATCTGTGCTTCCTTCAGAGATCATTTCAACCCGC 525
QY 498 GAGTTTCTGATCTCAATCTCGGCTTCGCCGCGAGTTTCTTACAAATTCAG 557
Db 526 CAGTTTGTGTGATTAATGATCTTGGCTCCCTGTGCTGCTGTTTACTTCAATTTGTCAG 585
QY 558 AGGAGAGTGTGCTGCGAGAGAAGACTTTAGATGCTT 597
Db 586 AGAGAGACTGCTGCCAGAGGCGCTGAAATTCAGATCTT 625

RESULT 15
AAC90668
ID AAC90668 standard; cDNA; 519 BP.
XX
AC AAC90668;
XX
DT 20-MAR-2001 (first entry)
XX
DE Strawberry flowering regulation protein coding sequence SEQ ID NO: 43.
XX
KM Strawberry; flowering regulation; floral homeotic gene; field crop;
XX
KW harvesting; fruit production; ss.
XX
OS Fragaria vesca.
XX
PN WO200071722-A1.
XX
PD 30-NOV-2000.
XX
PE 24-MAY-2000; 2000MO-US14297.
XX
PR 25-MAY-1999; 99US-0318789.
XX
PR 24-MAY-2000; 2000US-0318789.
XX
PA (DNAP) DNA PLANT TECHNOLOGY CORP.
XX
PI Oeller P, Guttererson N;
XX
DR WPI: 2001-025165/03.
XX
P-PSDB: AAB50271.
XX
PT Novel nucleic acid involved in controlling plant flowering processes is
PT useful for generating transgenic plants, in particular strawberry
PT plants having altered flowering behavior such as early, delayed or
PT day-neutral flowering
XX
PS Claim 23; Page 94-95; 97pp; English.
XX
CC The present invention provides the nucleic acid and protein sequences of
CC a number of proteins from the strawberry which are involved in the
CC regulation of flowering. These were identified using primers based on the
CC homologous sequences from A. thaliana, B. napus and R. sativus. They can
CC be used in the production of transgenic field crops whose flowering is
CC regulated and the time of fruiting and harvesting can be manipulated.
XX
SQ Sequence 519 BP; 143 A; 132 C; 120 G; 124 T; 0 other;

Query Match 18.8%; Score 161.2; DB 22; Length 519;
Best Local Similarity 57.9%; Pred. No. 3.6e-28;
Matches 286; Conservative 0; Mismatches 208; Indels 0; Gaps 0;

QY 71 AATATATAGAGACCTCTATAGTAAGAGAGTCTTGAGACCTTGTGATCCGTTAA 130
Db 6 AAGATGTCGAGACCTCTAGCTGTGGAAGATGATAGAGATGTTCTTGATCCCTCAC 65
QY 131 TAGATCAATCACTTAAGTCTTACTATGCGCAAGAGAGTGAATGCTTGATCT 190
Db 66 CCCACATCAAAATGATGTCTCTTCAACAGACGAGCTGCTGCAATGAGCATGAGCT 125

QY 191 AAGGCTTCGAGTTCAAAACAGCCAGAGTTGAGATGTGTGAGAGAAGACCTCAGAA 250
Db 126 CTTCCTTCTGACGACACCGCCAAACCTAGATGAGATTCAGAGGCGACATGATC 185
QY 251 CTTCATATCTTGGTTATGATGATGATCCAGATGTTCCAGTCTTACCAACCTCAG 310
Db 186 ATTCTTACTCTGGTAATGACAGACAGACGATGTTCTGCGCTTATGATCTTATTTGA 245
QY 311 AGATATCTCATCTGTTGTTGATGATGATATCCCTGCTACAACTGGAACACCTTTGCAA 370
Db 246 AGAGACCTGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 305
QY 371 TGAGATTTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 430
Db 306 AGAAGTGTGAGCTACGAGATGATGATGATGATGATGATGATGATGATGATGATG 365
QY 431 ATTTGTTGACAGCTTGGCAGGCAACAGTGTATGACACGAGGTTGCGCCAGAACTTCAA 490
Db 366 TCTCTTCAATGCAAAAGCAAGGACGATGATGATGATGATGATGATGATGATGATG 425
QY 491 CACTGCGAGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 550
Db 426 CACCGAATCTGCGAGCGGAAACGACCTTGTGTTCTGTTGCTGCTTACTTCAA 485
QY 551 TTGTGAGAGGAGA 564
Db 486 TGCACAGAGAGAAA 499

Search completed: May 2, 2003, 10:45:30
Job time : 289.5 secs

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 2, 2003, 05:54:34 ; Search time 1783.5 Seconds
(without alignments)
7773.107 Million cell updates/sec

Title: US-09-845-849-1

Perfect score: 856
Sequence: 1 tctgaactagtgatcccc.....aaaaaaaaaactcgag 856

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estm:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_tod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	516.4	60.3	518	10	AV563203
2	494	57.7	494	10	AV563277
3	423	49.4	423	10	AV788551
4	234	27.3	551	10	BE590867
5	231.6	27.1	659	14	BQ797327
6	206	24.1	206	10	AV560420

7	199.4	23.3	1168	11	AV11549	AV11549 Zea mays
8	198.4	23.2	505	10	BE498304	BE498304 WHE0963_B
9	196.8	23.0	491	12	BF483056	BF483056 WHE2314_C
10	184.6	21.6	542	10	AV937451	AV937451 AV937451
11	181	21.1	781	12	BG647258	BG647258 EST50867
12	173.2	20.2	718	13	BM407295	BM407295 EST581622
13	166.8	19.5	498	13	BJ453783	BJ453783 BJ453783
14	164	19.2	671	13	BJ448552	BJ448552 BJ448552
15	157.2	18.4	597	13	BJ315664	BJ315664 BJ315664
16	154.6	18.1	476	14	BQ518869	BQ518869
17	152.4	17.8	572	13	BJ461322	BJ461322 BJ461322
18	152.4	17.8	574	13	BJ456274	BJ456274 BJ456274
19	151.2	17.7	528	14	BM814255	BM814255 EST592348
20	150.8	17.6	395	17	BE558079	BE558079 BOGFM69TF
21	146.8	17.1	520	10	BE602964	BE602964
22	143	16.7	574	12	BF259482	BF259482 HVSME010
23	142.2	16.6	773	17	BH542868	BH542868 BOGJN29TF
24	141	16.5	459	9	AL385107	AL385107 MCB26D07
25	140.8	16.4	432	10	BE319228	BE319228 NF015E08R
26	139.4	16.3	580	13	BI478762	BI478762 949070A05
27	139	16.2	545	10	AM684982	AM684982 NF023H07N
28	136.8	16.0	545	13	BJ212200	BJ212200
29	132.6	15.5	383	10	AM927655	AM927655 945014B02
30	131.2	15.3	478	10	AM684071	AM684071 NF011G04N
31	127.6	14.9	543	10	AM284098	AM284098 LGL 267 G
32	127.2	14.9	558	13	BI426705	BI426705 sag07c12.
33	122.6	14.3	381	14	T44654	T44654 7917 Lambda
34	122.6	14.3	687	13	BI679012	BI679012 SWS105 S
35	116.2	13.6	463	10	AW707147	AW707147 sk10C07.Y
36	115.6	13.5	337	13	BI751372	BI751372 Taol1.16H0
37	114.2	13.3	417	12	BF473137	BF473137 WHE0522.A
38	113.8	13.3	357	13	BI941606	BI941606 sc77901.Y
39	113.2	13.2	682	13	BI311589	BI311589 EST531333
40	105	12.3	333	10	BE500873	BE500873 WHE0991-F0
41	103.2	12.1	608	12	BC463850	BC463850 EMI_51_F0
42	102.8	12.0	586	13	BM269830	BM269830 sak20H06.
43	101.6	11.9	341	13	BI750810	BI750810 Taol1.02c1
44	101.4	11.8	522	10	AM981994	AM981994 PC22E11 P
45	101.4	11.8	627	17	AQ289409	AQ289409 nbxD0035E

ALIGNMENTS

RESULT 1
LOCUS AV563203 518 bp mRNA linear EST 07-SEP-2000
DEFINITION AV563203 Arabidopsis thaliana green siliques Columbia Arabidopsis
thaliana cDNA clone S0183b01F 3', mRNA sequence.

ACCESSION AV563203
VERSION AV563203.1 GI:8734629
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
TITLE Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
1 (bases 1 to 518)

A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries

JOURNAL DNA Res. 7, 175-180 (2000)

MEDLINE 20363093

COMMENT

CONTACT: Erika Asamizu

The First Laboratory for Plant Gene Research

Kazusa DNA Research Institute

Yana 1532-3, Kisarazu, Chiba 292-0812, Japan

Email: asamizuekazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

Location/Qualifiers

1. 518

/organism="Arabidopsis thaliana"

/strain="Columbia"

FEATURES

source

```

/db_xref="taxon:3702"
/clone="SQ18301F"
/clone_lib="Arabidopsis thaliana green siliques Columbia"
/tissue_type="green siliques"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT      163 a      120 c      85 g      150 t
ORIGIN

```

Query Match	60.3%	Score 516.4	DB 10	Length 518
Best Local Similarity	99.8%	Pred. No. 1.9e-79		
Matches 517; Conservative	0	Mismatches 1	Indels 0	Gaps 0

OY	312	GAATATCTCCAAATGGTGTGGTGCATATATCCCTGCTACAAACGTGGAACAACCTTTGGCAAT	371
Dd	518	GNATTCCTCCAAATGGTGTGGTGCATATATCCCTGCTGCACACGTGAACAACCTTTGGCAAT	459
OY	372	GAGATTTGTGTGTATTACGAAAAATCCAAAGTCCCACTGCAGCAAAATTCATCTGTGCTGTTTATA	431
Dd	458	GAGATTTGTGTGTATTACGAAAAATCCAAAGTCCCACTGCAGCAAAATTCATCTGTGCTGTTTATA	399
OY	432	TTGTTTGCACAGCTTGGGAGGCAACAGTGTATGTGACACAGGGTGGGCGCCAGAACTTCAAC	491
Dd	398	TTGTTTGCACAGCTTGGGAGGCAACAGTGTATGTGACACAGGGTGGGCGCCAGAACTTCAAC	339
OY	432	ACTCGCAGATTGCTGAGATCTACAAATCTCGGCCCTCCCGTGGCGCCGACATTTTCTACAAT	551
Dd	338	ACTCGCAGATTGCTGAGATCTACAAATCTCGGCCCTCCCGTGGCGCCGACATTTTCTACAAT	279
OY	552	TGTCGAGAGGAGAGGCGGCGGAGAGAAACATTTTGATGGGCTTCCTCCCTTTAAAC	611
Dd	278	TGTCGAGAGGAGAGGCGGCGGAGAGAAACATTTTGATGGGCTTCCTCCCTTTAAAC	219
OY	612	AATTCGATATTCGATCTCTGATGAGATTTATGCATCTATAGTATTTTAAATTTAAATTAACCA	671
Dd	218	AATTCGATATTCGATCTCTGATGAGATTTATGCATCTATAGTATTTTAAATTTAAATTAACCA	159
OY	672	TTTTTATGATAGAGTAACGAACGCGGATGATGCCATAGTAACTTCAATATATAAGTGT	731
Dd	158	TTTTTATGATAGAGTAACGAACGCGGATGATGCCATAGTAACTTCAATATATAAGTGT	99
OY	732	AATAAAATGAGAGGGGAGGCAAAATGAGAGGTTTACTATATAGTGTGATGCCAT	791
Dd	98	AATAAAATGAGAGGGGAGGCAAAATGAGAGGTTTACTATATAGTGTGATGCCAT	39
OY	792	AATATATATTAATCTATCATGAATAATGAAGTGTATATTTA	829
Dd	38	AATATATATTAATCTATCATGAATAATGAAGTGTATATTTA	1

RESULT 2	AV562377/c	LOCUS	AV562377	494 bp	mRNA	linear	EST 07-SEP-2000
DEFINITION	AV562377	Arabidopsis thaliana green siliques Columbia	thaliana cDNA clone SQ169B07F 3'				Arabidopsis mRNA sequence.

VERSION	AV562377.1	GI:8733803
KEYWORDS	EST.	
SOURCE	thale cress.	
ORGANISM	Arabidopsis thaliana	

REFERENCE AUTHORS TITLE
1 (bases 1 to 494) Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S. A large scale analysis of cDNA in Arabidopsis thaliana: Generation

JOURNAL DNA Res. 7, 175-180 (2000)
MEDLINE 20032003

COMMENT

The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute

FEATURES
source
1. .494
location/Qualifiers
Email: asami@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan

```

/tissue_type="green silques"
/notes="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"

```

BASE COUNT	155 a	113 c	81 g	145 t
ORIGIN				

Query Match	Similarity	57.7%	Score 494	DB 10	Length 494
Match	Local Similarity	100.0%	Pred. NO. 1.4e-75		
Matches	494	Conservative	0	Mismatches	0
				Indels	0
				Gaps	0
QY	335	TGATATCCCTGCTACAACTGAAACAACCTTTGGCAGATGAGATTGTTGTATACGAAATCC	394		
Db	494	TGATATCCCTGCTACAACTGAAACAACCTTTGGCAGATGAGATTGTTGTATACGAAATCC	435		
QY	395	AAATCCCACTGACAGAAATTCATCGTGTGTGTTTATTTGTTTCACACAGCTTGGCAGGCA	454		
Db	434	AAATCCCACTGACAGAAATTCATCGTGTGTGTTTATTTGTTTCACACAGCTTGGCAGGCA	375		
QY	455	AACAGTGTATGCACACAGAGGTGGCGCCAGAACCTTCACAACTCGCAGATTGCTGAGATCTA	514		
Db	374	AACAGTGTATGCACACAGAGGTGGCGCCAGAACCTTCACAACTCGCAGATTGCTGAGATCTA	315		
QY	515	CAATCTGGCCCTTCCCGTGCCGCGCAGTTTCTACAAATGTGTCAGAGGAGAGTGCCTGGG	574		
Db	314	CAATCTGGCCCTTCCCGTGCCGCGCAGTTTCTACAAATGTGTCAGAGGAGAGTGCCTGGG	255		
QY	575	AGGAAGAAGACTTTAGATGGCTTCTTCCCTTATTAACCAATGTATTTGCATCTCTGATG	634		
Db	254	AGGAAGAAGACTTTAGATGGCTTCTTCCCTTATTAACCAATGTATTTGCATCTCTGATG	195		
QY	635	AGATTATGCACTCTATAGCTAATTTTAATTAATAACCAATTTTATGATAGAGTAACGACG	694		
Db	194	AGATTATGCACTCTATAGCTAATTTTAATTAATAACCAATTTTATGATAGAGTAACGACG	135		
QY	695	GTGATGATGCTATAGTAGTCAATATATTAAGTGTGTATATAAATAAGAGGGGAGGAA	754		
Db	134	GTGATGATGCTATAGTAGTCAATATATTAAGTGTGTGTATATAAATAAGAGGGGAGGAA	75		
QY	755	AATGAGAGTGTATTAATTAATAGTGTGATGCGATTAATTAATTAATTAATTAATTAATTAAT	814		
Db	74	AATGAGAGTGTATTAATTAATAGTGTGATGCGATTAATTAATTAATTAATTAATTAATTAAT	15		
QY	815	GAAGCTATATATTT 828			
Db	14	GAAGCTATATATTT 1			

RESULT 3	LOCUS	423 bp	mrna	linear	EST 28-MAR-2002
AV788551/c	AV788551				
DEFINITION	RAFL6 Arabidopsis thaliana cDNA clone RAFL6-80-B19 3'				

KEYWORDS	EST:
SOURCE	thale cress.
ORGANISM	<i>Arabidopsis thaliana</i>

Rosidae; euros

REFERENCE

Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.

TITLE and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
JOURNAL Unpublished (2002)
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msek@rcc.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). This clone is in a modified pBluescript vector as a SstI/XhoI insert. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES

source
Location/Qualifiers
1..423
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone="RAF106-80-B19"
/clone_lib="RAF16"
/dev_stage="plants at various developmental stages from germination to mature seeds"
/lab_host="DH10B"
/note="Site: 1: SstI; site: 2: XhoI; subjected to dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24 hr) treatments"
BASE COUNT 131 a 99 c 70 g 123 t
ORIGIN
Query Match 49.4%; Score 423; DB 10; Length 423;
Best Local Similarity 100.0%; Pred. No. 2.4e-63;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

382 GTTACGAAATCCAGTCCACGACGAGAAATCATCGTGTGTTATATGTTTCGAC 441
|||||
423 GTTACGAAATCCAGTCCACGACGAGAAATCATCGTGTGTTATATGTTTCGAC 364
|||||
442 AGCTGGCAGCAAGAGTATGACGAGGCGCCAGCACTTCAACACCTCCGAGT 501
|||||
363 AGCTGGCAGCAAGAGTATGACGAGGCGCCAGCACTTCAACACCTCCGAGT 304
|||||
502 TTCTGAGATCTCAATCTCGGCTTCCGCGCGCAGTCTTCAATTTGTCAGAGG 561
|||||
303 TTCTGAGATCTCAATCTCGGCTTCCGCGCGCAGTCTTCAATTTGTCAGAGG 244
|||||
562 AGAGTGCTCGGAGCAAGACTTATAGTGGCTTCTCTTATTAACCAATGATATT 621
|||||
243 AGAGTGCTCGGAGCAAGACTTATAGTGGCTTCTCTTATTAACCAATGATATT 184
|||||
622 GCATCTCTGATGATATTTGATATGATATTTAATTAATTAACCAATTTATGATA 681
|||||
183 GCATCTCTGATGATATTTGATATGATATTTAATTAATTAACCAATTTATGATA 124
|||||
682 CGAGTACGAAAGCGTATGATGCTATAGTATGATTAATTAATTAATTAATTAAT 741
|||||
123 CGAGTACGAAAGCGTATGATGCTATAGTATGATTAATTAATTAATTAATTAAT 64
|||||
742 AGAGGGGAGGAAATGAGAGTGTCTTATTAATTAATTAATTAATTAATTAATTA 801
|||||
63 AGAGGGGAGGAAATGAGAGTGTCTTATTAATTAATTAATTAATTAATTAATTA 4
|||||
802 ATC 804
|||
3 ATC 1

RESULT 4
BE590867 551 bp mRNA linear EST 18-AUG-2000
LOCUS BE590867
DEFINITION WHE0855_C01_E0125 wheat 20-45 DAP spike cDNA library Triticum
aestivum cDNA clone WHE0855_C01_E01, mRNA sequence.
ACCESSION BE590867

VERSION BE590867.1 GI:9845940
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum

REFERENCE
AUTHORS Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Iazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Tong, J.C.
TITLE The structure and function of the expressed portion of the wheat genomes - 20-45 DAP spike cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105959773
Fax: 5105959818
Email: oanderson@w.usda.gov

Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: StrataGene SR primer.

FEATURES

source
Location/Qualifiers
1..551
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE0855_C01_E01"
/clone_lib="Wheat 20-45 DAP spike cDNA library"
/tissue_type="Spoke and seed"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site: 1: EcoRI; Site: 2: XhoI; Plants were grown in the greenhouse. Spikes at 20 DAP and seeds at 30 to 45 DAP were harvested, total RNA and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)"

BASE COUNT 106 a 171 c 168 g 106 t
ORIGIN
Query Match 27.3%; Score 234; DB 10; Length 551;
Best Local Similarity 68.9%; Pred. No. 6.2e-31;
Matches 321; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

78 AGAGACCCCTCTTATAGTACGAGAGTGTGGAGACGTTCTGATCCGTTAATGATCA 137
|||||
85 AGAGACCCGCTGTGTGGAGGTTGTGGGAGACGTTCTGATCCGTTAATGATCA 144
|||||
138 ATCACTCTAAGGTTACTTATAGCCAAAGAGAGTATGCTGATGATCTAAGGCT 197
|||||
145 ACCAAGCTCAGGAGTCTTGGAGACAGACCGTGTCCACGCGTGGAGCTCAAGCG 204
|||||
198 TCTCAGGTTCAAAACAGCCAGAGTTGAGATTGGTGGAGAGACCTCAGCACTTCTAT 257
|||||
205 TCCATGGTCCGCCAGACGCCAGAGGTTGAGGTGGCGGCATGAGATGAGAGACTTCTAC 264
|||||
258 ACTTTGGTATGATGATCCAGATGTTCCAGTCTTCAACCTCAGCTCCGAGATAT 317
|||||
265 ACACCTCGTATGATGATCCAGATGTTCCAGTCTTCAACCTCAGCTCCGAGATAT 324
|||||
318 CTCATGTTGTTGATGATCCGCTGCTACCTGAGAACCTTGGCAATGAGATT 377
|||||
325 CTCACATGCTGTGTGATGATATCCCGGTACCACTGATGATCTTCCGCGCAGAGAGTG 384
|||||
378 GTGTGTACGAAATCCAGTCCACGTCAGGAATTCATCGTGTCTTATTAATTTGTTT 437
|||||

Db 385 ATGTCTACGAGAGCCCTGTCGACCAATGGGATCATCTGCTGCTGCTCTTC 444
QY 438 CGACAGCTTGGAGCAAAAGATGTATGACACAGAGGTGGCGGACAGCTTCAACACTGC 497
Db 445 CAGCAGCTCGGCGGACAGACCGGTGTACGCTCCCGGTGGCGGACAGATTCAACACGAG 504
QY 498 GAGTTTGGTGAATCTACAAATCTGGGCTTCCTCCGTGGCGGAGTTT 543
Db 505 GACCTCGCGGAGCTCTACACCTCGGCGGCTGCTGCGGCGCTCT 550

RESULT 5
BQ797327/c 659 bp mRNA linear EST 30-JUL-2002
LOCUS EST 6265 Ripening Grape berries lambda zap II library Vitis
DEFINITION Vitis vinifera cDNA clone RT071D11 3', mRNA sequence.
ACCESSION BQ797327.1 GI:22012293
VERSION BQ797327.1
KEYWORDS EST.
SOURCE Vitis vinifera.
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Vitaceae; Vitis.
REFERENCE 1 (bases 1 to 659)
AUTHORS Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
CONTACT: Romieu C.
JOURNAL Institut National de la Recherche Agromique
COMMENT 2, place Viala, 34 060 Montpellier Cedex 01, France
Tel: 00-33-(0)4-99-61-28-62
Fax: 00-33-(0)4-99-61-28-57
Email: romieu@enscm.inra.fr
Seq primer: T7.

FEATURES
source Location/Qualifiers
1..659
/organism="Vitis vinifera"
/cultivar="Shiraz"
/db_xref="taxon:29760"
/clone="RT071D11"
/clone_lib="Ripening Grape berries lambda zap II library"
/dev_stage="ripening stage"
/note="Organ: Fruit; Vector: lambda zap II; Site_1: Eco RI
; Site_2: XhoI; Oriented library, construction described
in Generation of ESTs from grape Berry (skin, pulp or
seeds) at various developmental stages by Terrier,N.,
Ageorges,A., Abbal,P., Romieu,C. In J. Plant Physiol. 158
(12): 1575-83 2001"

BASE COUNT 197 a 155 c 124 g 183 t
ORIGIN
Query Match 27.1%; Score 231.6; DB 14; Length 659;
Best Local Similarity 74.6%; Pred. No. 1.5e-30;
Matches 291; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

Db 479 GTTATATAGAGCCACCCACAGCTGGAGTTTCATGCTTTGTTATGTTTCG 420
QY 440 ACAGCTTGGAGCAAAAGATGTATGACACAGAGGTGGCGGACAGACTTCAACACTGC 499
Db 419 CCAACTGGTATGGAGACAGTGTATGACACAGAGGTGGCGGCAAAATTTCAACACTAGGGA 360
QY 500 GTTTCCTGAGATCTCAATCTCGGCTTCGCGTGGCGGAGTTTCTCAATTTGTACAG 559
Db 359 CTTTCTAGAGCTTTATATCTGTTGCTTGTCTGCTGCTGTTTAACTGCCAAG 300

QY 560 GGAGAGTGGCTGCGGAGACAGACTTTA 589
Db 299 GGAGGCGGCTCGGCTGCTGCAAGATCATTA 270

RESULT 6
AV560420/c 206 bp mRNA linear EST 07-SEP-2000
LOCUS AV560420 Arabidopsis thaliana green siliques Columbia Arabidopsis
DEFINITION thaliana cDNA clone SQ134D05F 3', mRNA sequence.
ACCESSION AV560420
VERSION AV560420.1 GI:8731846
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1 (bases 1 to 206)
AUTHORS Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)

JOURNAL Contact: Erika Asamizu
COMMENT The First Laboratory for Plant Gene Research
MEDLINE Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

FEATURES
source Location/Qualifiers
1..206
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="SQ134D05F"
/clone_lib="Arabidopsis thaliana green siliques Columbia"
/tissue_type="green siliques"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 69 a 43 c 28 g 66 t
ORIGIN
Query Match 24.1%; Score 206; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 6.4e-26;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 7
LOCUS AY111549 1168 bp mRNA linear HTC 26-MAY-2002
DEFINITION Zea mays CU846_1 mRNA sequence.
ACCESSION AY111549
VERSION AY111549.1 GI:21216139
KEYWORDS HTC.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PAC
Clade; Panicoidae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1168)
AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hainey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/Dupont Consensus Sequences for Design of
Overgo Probes
TITLE Unpublished (2002)
JOURNAL 2 (bases 1 to 1168)
REFERENCE Coe,E.C.
AUTHORS Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
FEATURES
source
1.1168
/organism="Zea mays"
/db_xref="MaizeDB:532948"
/db_xref="taxon:4577"
/clone="Cl846.1"
/clone_lib="Maize Mapping Project/Dupont Consensus
Library"
/note="this sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed Dupont contigs; this resource was
assembled by Dupont as part of a collaboration for the
overgo addressing of BACS in conjunction with the Maize
Mapping Project"
BASE COUNT 181 a 247 c 245 g 159 t 336 others
ORIGIN
Query Match 23.3%; Score 199.4; DB 11; Length 1168;
Best Local Similarity 48.4%; Pred. No. 3.8e-25;
Matches 302; Conservative 0; Mismatches 322; Indels 0; Gaps 0;
0;
78 AGAGACCTCTTATAGTACGAGAGTGTGAGACGCTTCTGATCCGTTTATATAGATCA 137
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
190 AGGAGAGCCGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 249
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
138 ATGACTCTAAGGTTACTTATGCGCAAGAGAGTGACTATAGCTTGATCTTAAGCCT 197
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
250 ACCAACTCAGGCTCAGCTACGAGGCGGCGGAGACCGTGTCAAGCGCTCAAGCCG 309
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
198 TCTCAGGTTCAAAACAGCAAGAGTGAAGATTGGTGAGAGAAGACCTCAGGAACCTTCTAT 257
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
310 TCCATGCTGTGTCACACGAGGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 369
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
258 ACTTTGGTATGTTGATCCAGATGTTTCAAGTCTCAGCAACCTCCTCCGAGAAATAT 317
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
370 ACCCTGCTGATGTTGAGCCGAGATGCTCGAGCCCAAGCCGAGACCTTAGAGAGTAT 429
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
318 CTCATGTTGTTGTTGATGATATCCCTGCTACAACTGGAACACCTTTGGCAATGAGATT 377
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
430 CTACACTGGGTGTGAGATATTCGGAACACTGAGGAGAGATTGGCAGAGAGTG 489
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
378 GTGTGTTGCAAAATCCAAATCCACAGCAAGTATGCTGCTGTTATATGTTT 437
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
490 ATCTGTACAGAGAGCCCTCGGCGGAGATGATCCACGCTTCGTGCTGCTTTC 549
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
438 CGACAGCTTGAGAGCAAGAGATGATGACACAGAGTGCGGCGGAGAACTTCACACATCGC 497
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
550 CACACAGCTGGGCGGCGGAGAGAGTGTGAGCCCGGCTGGCGGCGGAGAACTTCACACACAGG 609
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

```

```

QY 498 GAGTTTCTGAGATCTACATCTCGCCCTTCCCGCCGAGTTTCTACATTTGACAG 557
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 610 GACTTCGCCGAGCTCTACNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 669
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
QY 558 AGGAGAGTGGCTCGCGGAGAGAGACTTATGATGGCTTCTCTTATACCAATTGA 617
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 670 CGTAGAGCCGGCTCTNNNNNNCAGAGGNNNNNNNNNNNNNNNNNNNNNNNNNNNN 729
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
QY 618 TATTGACTACTCTGATGAGATTTATGATCTATGATATTTAATTATACATTATAT 677
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 730 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 789
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
QY 678 GATACGAGTACGACGCTGATGA 701
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 790 TCGTCACTACTCAACATATACGA 813
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
RESULT 8
LOCUS BE498304 505 bp mRNA linear EST 04-AUG-2000
DEFINITION WHE0963_B10.C192S wheat pre-anthesis spike cDNA library Trilicium
aestivum cDNA clone WHE0963_B10.C19, mRNA sequence.
ACCESSION BE498304
VERSION BE498304.1 GI:9697017
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Trilicium aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Triticum.
1 (bases 1 to 505)
REFERENCE Anderson,O.D., Cho,S., Choi,D.M., Close,T.J., Fenton,R.D., Han
AUTHORS P.S., Hala,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J.,
Seaton,C.L. and Tong,J.C.
TITLE The structure and function of the expressed portion of the wheat
genomes - Pre-anthesis spike cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105959773
Fax: 5105595818
Email: oanderson@wv.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
FEATURES
source
1.505
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE0963_B10.C19"
/clone_lib="Wheat pre-anthesis spike cDNA library"
/tissue-type="Spike before anthesis"
/dev-stage="Adult plant"
/lab-host="E. coli SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Plants were grown in the
greenhouse. Whole spike with awns trimmed, white, green
and yellow anther were collected and total RNA, and
poly(A) RNA were prepared, a cDNA library was made, and
the cDNA clones were in vivo excised to give plasmid
phagemids in the T7 Close lab (Choi, Close, Fenton) at
the University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
BASE COUNT 99 a 148 c 160 g 98 t
ORIGIN
Query Match 23.2%; Score 198.4; DB 10; Length 505;
Best Local Similarity 67.3%; Pred. No. 8.4e-25;

```


Db 258 CTTGGAACAACGTGTGCGAGCTTGCGCGAGAGCTTGATTTTGAAGAAGACAGAAACA 317
 Oy 402 ACTGACAGAAATTCATCGTGTGCTTTATATATTTTGACAGCTTGGCAGCAACAAGATG 461
 Db 318 AGATCTGTATTCACCGGATGATTTGTGCTGTTCCAGCAACATGAGGAGGATACATT 377
 Oy 462 TATGACACAGGTTGGCGCAGCAACTTCAACACTCGCGAGTTGGTGAATATCAATATTC 521
 Db 378 TTTCACACAGACGTCGCCAACAACTTCAAGCTGCGAGAACTTGTACAGCAATACACCTA 437
 Oy 522 GGCCTTCCCTGGCCGAGTTTCTACAAATTTGAGAGGAGAGTGGCTGGGAGAGAA 581
 Db 438 AACGT---GTGCTGCTCATATTTCAACTGTCAAGGAGAGTGATTCAGGGGAGAA 494
 Oy 582 AG 583
 Db 495 AG 496

RESULT 14

BJ448552

LOCUS BJ448552 671 bp mRNA linear EST 23-MAY-2002
 DEFINITION BJ448552 K. Sato unpublished cDNA library, cv. Akashinriki
 vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone
 bakx20f16 5', mRNA sequence.

ACCESSION

BJ448552

VERSION

BJ448552.1

KEYWORDS

EST.

SOURCE

Hordeum vulgare subsp. vulgare.

ORGANISM

Hordeum vulgare subsp. vulgare

REFERENCE

1 (bases 1 to 671)

AUTHORS

Sato, K., Saisyo, D. and Takeda, K.

TITLE

Barley EST sequencing project in NIG and Okayama Univ

JOURNAL

Unpublished (2002)

COMMENT

Contact: Tadasu Shin-i

FEATURES

Location/Qualifiers

1..671

/organism="Hordeum vulgare subsp. vulgare"

/cultivar="Akashinriki"

/db_xref="taxon:112509"

/clone="bakx20f16"

/clone_id="K. Sato unpublished cDNA library, cv.

Akashinriki vegetative stage leaves"

/tissue_type="leaves"

/dev_stage="vegetative stage"

BASE COUNT 189 a 142 c 166 g 173 t 1 others

ORIGIN

Query Match 19.2%: Score 164; DB 13; Length 671;

Best Local Similarity 60.5%; Pred. No. 6e-19;

Matches 288; Conservative 0; Mismatches 185; Indels 3; Gaps 1;

Oy 112 ACCTTTCGATCCGTTTATATGATCAATCACTTAAGGTTACTTATGCGCCAAAGAGAGG 171

Db 29 ATGTGCTTGATCATTTACATCAACCGTTCATTAGATAGCTTACAAACATAGGCTAG 88

Oy 172 TGACTAATGCTTGATCAAGGCTTCTCAGTTTCAAAACAGCAAGAGTGTGAGATTG 231

Db 89 TTTCGACAGGCTGTGAGCTTAAGACCATCTGCAATTTGTAAGTACGACGAGTTGATTTG 148

Oy 232 GTGAGAGAGACCTCAGGAATCTTATACCTTTGTTATGTTGATCCAGATCTTCCAACTC 291

Db 149 GTGCGAGTACATAGAGTTCTACACACCGTATATGTTGTTGATCCAGACGCTCCAAAGCC 208

Oy 292 CTAGAACCTTCACCTCCGAGAAATATCTCATTTGGTTGGTGAATATATCCCTGTACAA 351
 Db 209 CAGTACACCTTCATCAATAGGAGTACTTGTGATGTGTGATGTGTGATGTGTGATGTGTG 268
 Oy 352 CTGGAACACCTTTGGCAATGAGATTTGTGTGATGAGAAATCAAGTCCACATCAGAA 411
 Db 269 CTGGTGCCAGCTGTGGCCGAGAGCTTTGATTTATGAAAGACAGAACCAAGATCTGTGA 328
 Oy 412 TTTCATGCTGTGTGTTTATATTTTTCAGACCTTTGGCAGCAACACATGTATGACCA 471
 Db 329 TCCACCGGATGATTTTGTGCTGTTCCAGCACTAGGAGGATACATTTTGTGACCA 388
 Oy 472 GGTGGCGCAGACACTTCAACACTCGCGAGTTTGTGATGTGATGTGATGTGATGTGAT 531
 Db 389 ACCTCCGACAAACTTCAAGCTGCGAGAACTTTGCAAGCAGTACCACTTAACGTT---G 445
 Oy 532 TGGCGCAGTTTCTACAAATTTGTCAGAGGAGAGTGGCTGGGAGAGAAAGACTT 587
 Db 446 TGGCTGCTCATATTTTCAACTGTCAAGGAGAGTGTGATCAGCGGAGAGGATT 501

RESULT 15

BJ315664

LOCUS BJ315664 597 bp mRNA linear EST 09-APR-2002
 DEFINITION BJ315664 Y. Ogihara unpublished cDNA library, Wh_yf Triticum
 aestivum cDNA clone whyf19117 5', mRNA sequence.

ACCESSION

BJ315664

VERSION

BJ315664.1

KEYWORDS

EST.

SOURCE

bread wheat.

ORGANISM

Triticum aestivum

REFERENCE

1 (bases 1 to 597)

AUTHORS

Ogihara, Y. and Murai, K.

TITLE

Expressed genes in Triticum aestivum

JOURNAL

Unpublished (2002)

COMMENT

Contact: Tadasu Shin-i

FEATURES

Location/Qualifiers

1..597

/organism="Triticum aestivum"

/cultivar="Chinese Spring"

/db_xref="taxon:4565"

/clone="whyf19117"

/clone_id="Y. Ogihara unpublished cDNA library, Wh_yf"

/tissue_type="spikelet at early flowering"

/dev_stage="Peekes' scale 6"

/note="Vector: lambda Uni-ZAP XR, excised phagemid;

Site_1: EcoRI; Site_2: XhoI; Plants were grown under

hydroponic conditions at UC Davis, salt stressed for 12

hours, and for 7 days, then dissected and frozen (Akhunov

in J Dvorak lab). Total RNA was prepared from sheath

tissue, equal quantities of RNA were pooled from the two

samples, polyA was purified from the pooled RNA, a cDNA

library was made, and the cDNA clones were in vivo

excised to give plasmid phagemids in the T7 Close lab

at the University of California, Riverside (Akhunov, Chin

, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).

Plasmid DNA preparations and DNA sequencing were

performed in the OD Anderson lab (all other authors)."

BASE COUNT 153 a 151 c 143 g 147 t 3 others

ORIGIN

Query Match 18.4%: Score 157.2; DB 13; Length 597;

Best Local Similarity 59.0%; Pred. No. 9.4e-18;

Matches 289; Conservative 0; Mismatches 198; Indels 3; Gaps 1;

OY	81	GACCCCTTTATAGTAAGACAGTGTGGAGACGCTCTTATCCGTTATTAATAGTCAATC	140
Db	83	GAACCTCTTATTTGGGGGGGGGTATTGGAGAAAGTTCTTGATACATTAAACCATGTGTG	142
OY	141	ACTCTAAAGGTTACTTATGAGCCAAAGAGAG--GTGACTAATAGGCTTGGATCTAAGGCGCT	197
Db	143	AAGATGGTAAGACCTATTAACTCCAAACAGCTTGTCTTCAATGGCCATGAGCTCTACCCA	202
OY	198	TCTAGAGTTCAAAACAGGCCCAAGAGTTGAGTGTGGTGGAAAGACCCACAGAACTCTAT	257
Db	203	TCAGCGGTTGATCTAAACACGAGTGAAGGTCCCAAGGGGTGACTTGGCATCTTGTTTC	262
OY	258	ACTTGGTTATGTGGATCCAGATGTTCCAAAGTCCTAGCAACCCCTCAGCTCGAGATAAT	317
Db	263	ACACGCGTTATGACAGACCCCTGAATGTGCCAGGGCCAATGATCATATCTAAAGGAGCAC	322
OY	318	CTCCATTTGGTGGAGCTGATATCCCGTACCTGTCACATCGAAGCAACCTTGGCATAGATTT	377
Db	323	CTTCACCTGATTTGTTACTGATATATACCTGGGACACACAGATGCTTTTGGACGGGAATC	382
OY	378	GTTGTTTACGAAAAATCCAAAGTCCACATGCAAGGAATTCATGTCGTGTTTATATTGTTT	437
Db	383	ATAAGCTTATGAGACCCCAAAACCCAAATATGAGCATTCACAGAGTTTATTTTGTGCTCTTC	442
OY	438	CGACAGCTTGGCAGGCAAAACAGTATGCAACACAGGGTGGGGCCACAGACTTCAACACTCGC	497
Db	443	AAGCAGGAAGCGAAGGCAAGACTGTAACGTGTGCTTCTTCAAGGGATCATTTTCAACACCCCGT	502
OY	498	GAGTTTGGCTGAGATCTCAATATCTTGCGCTTCCGTTGGCCGACAGTTTCTCAATTTGTCAG	557
Db	503	CAGTTTGGCTGGAGAAATGACCTCGGCTCCCTGTGCACTGTGTCATCTCAACTGTCAAG	562
OY	558	AGGGAAGAGTG 567	
Db	563	AGGGAAGAGTG 572	

Search completed: May 2, 2003, 11:50:30
Job time : 1791.5 secs

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 1, 2003, 15:58:02 ; Search time 60 seconds
(without alignments)
4375.255 Million cell updates/sec

Title: US-09-845-849-1

Perfect score: 856
Sequence: 1 tctagaactagtgatgccccc.....aaaaaaaaaaaactgcgag 856

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.NA:*
1: /cgn2_6/prodata/1/lna/5A.COMB.seq:*
2: /cgn2_6/prodata/1/lna/5B.COMB.seq:*
3: /cgn2_6/prodata/1/lna/6A.COMB.seq:*
4: /cgn2_6/prodata/1/lna/6B.COMB.seq:*
5: /cgn2_6/prodata/1/lna/PCROS.COMB.seq:*
6: /cgn2_6/prodata/1/lna/Backfillseq1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	856	100.0	856	4	US-09-060-726A-3
2	842.4	98.4	855	4	US-09-060-726A-1
3	71.8	8.4	822	1	US-07-644-372-1
C 4	47	5.5	2185	2	US-08-467-948A-3
5	47	5.5	2185	2	US-08-467-947A-3
6	46.8	5.5	234	1	US-08-485-455D-60
7	46.8	5.5	234	2	US-08-482-130C-60
8	46.8	5.5	234	2	US-08-484-211C-60
9	46.8	5.5	234	3	US-08-906-769-60
10	46.8	5.5	234	3	US-08-906-616-60
11	46.8	5.5	234	3	US-08-817-795-60
12	46.8	5.5	234	3	US-08-485-443B-60
13	46.8	5.5	234	3	US-08-639-075A-60
14	46.8	5.5	234	4	US-09-012-431-60
15	46.8	5.5	234	4	US-09-012-692-60
16	46.8	5.5	234	4	US-08-906-613-60
17	46.8	5.5	234	5	PCR-US85-14442A-60
18	45.6	5.3	1601	1	US-07-968-971A-10
19	45.6	5.3	1601	1	US-08-424-406-6
20	45.4	5.3	2503	1	US-08-472-934-3
21	45.4	5.3	2503	1	US-08-472-934-11
22	45.4	5.3	2503	2	US-08-323-460A-3
23	45.4	5.3	2503	2	US-08-461-146C-3
24	45.4	5.3	2503	2	US-08-461-146C-11
25	45.4	5.3	2503	3	US-08-461-145C-3
26	45.4	5.3	2503	3	US-08-461-145C-11
27	45.4	5.3	2503	4	US-08-628-829-5

28	45.4	5.3	2503	4	US-08-628-829-7	Sequence 7, Appl1
29	45	5.3	1585	4	US-09-183-861-54	Sequence 54, Appl1
30	45	5.3	1585	4	US-09-022-765-54	Sequence 54, Appl1
31	44.8	5.2	897	4	US-08-899-330-14	Sequence 14, Appl1
32	44.8	5.2	3328	4	US-08-960-048-1	Sequence 14, Appl1
33	44.6	5.2	545	4	US-09-227-357-125	Sequence 125, Appl1
34	44.4	5.2	866	4	US-09-257-179-11	Sequence 11, Appl1
35	43.8	5.1	1058	4	US-08-818-112-14	Sequence 14, Appl1
36	43.8	5.1	1058	4	US-08-818-111-14	Sequence 14, Appl1
37	43.8	5.1	1058	4	US-09-056-556-14	Sequence 14, Appl1
38	43.8	5.1	1058	4	US-09-072-596-14	Sequence 14, Appl1
39	43.8	5.1	2775	4	US-08-730-771-1	Sequence 1, Appl1
40	43.8	5.1	2775	4	US-09-060-208-1	Sequence 1, Appl1
41	43.6	5.1	860	1	US-08-181-271A-33	Sequence 33, Appl1
42	43.6	5.1	860	1	US-08-449-315-33	Sequence 33, Appl1
43	43.6	5.1	860	1	US-08-444-803-33	Sequence 33, Appl1
44	43.6	5.1	860	1	US-08-449-043-33	Sequence 33, Appl1
45	43.6	5.1	860	1	US-08-456-265A-33	Sequence 33, Appl1

ALIGNMENTS

```
RESULT 1
US-09-060-726A-3/C
; Sequence 3, Application US/09060726A
; Patent No. 6225530
; GENERAL INFORMATION:
; APPLICANT: Weigel, Detlef
; APPLICANT: Salk Institute
; TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY
; MODIFIED PLANTS HAVING MODULATED FLOWER DEVELOPMENT
; FILE REFERENCE: SALKINS.026A
; CURRENT APPLICATION NUMBER: US/09/060.726A
; CURRENT FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 856
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-060-726A-3

Query Match      100.0%; Score 856; DB 4; Length 856;
Best Local Similarity 100.0%; Pred. No. 3e-217;
Matches 856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTAGACTAGTGGATCCCGGGCTGCAGGAATTCAGCAGAGTTGTTCAAGATCAA 60
    |||||||
DB 856 TCTAGAACTAGTGGATCCCGGGCTGCAGGAATTCAGCAGAGTTGTTCAAGATCAA 797
    |||||||

QY 61 AGATGCTATAAATATTAAGACCCCTTATAGTAAAGAGTTGAGACGCTTGG 120
    |||||||
DB 796 AGATGCTATAAATATTAAGACCCCTTATAGTAAAGAGTTGAGACGCTTGG 737
    |||||||

QY 121 ATCGTTTATAGTCAATCACTTAAGGTTACTTATGCGCAAGAGAGTACTATG 180
    |||||||
DB 736 ATCGTTTATAGTCAATCACTTAAAGGTTACTTATGCGCAAGAGAGTACTATG 677
    |||||||

QY 181 GCTTGATTAAGGCTTTCAGGTTCAAAACCAAGAGTTGATGGTGAAGAAG 240
    |||||||
DB 676 GCTTGATTAAGGCTTTCAGGTTCAAAACCAAGAGTTGATGGTGAAGAAG 617
    |||||||

QY 241 ACTCAGGAACCTTATATCTTGTATGTTGATGCCAGATGTTCCAAAGTCTAGCAACC 300
    |||||||
DB 616 ACTCAGGAACCTTATATCTTGTATGTTGATGCCAGATGTTCCAAAGTCTAGCAACC 557
    |||||||

QY 301 CTACACCTCCAGAAATATCTCATGTTGTTGATGATGATATCCGTTACAAAGTGAACAA 360
    |||||||
DB 556 CTACACCTCCAGAAATATCTCATGTTGTTGATGATGATATCCGTTACAAAGTGAACAA 497
    |||||||

QY 361 CCTTTGCAATGAGATGTGTGTATGACAAATCCAAATCCCACTGACGATATCATCGTG 420
    |||||||
```

Db 496 CCTTGGCAATGATGTTGTGTACGAAATCCAAATGCCACTGAGGAATTCATGCG 437
OY 421 TCGTGTATATATGTTTTCACAGCTTGGCAGCAACAGTATGACACGAGGTGGCGC 480
Db 436 TCGTGTATATGTTTTCACAGCTTGGCAGCAACAGTATGACACGAGGTGGCGC 377
OY 481 AGAAGCTTCAACCTGCGGAGTTGCTGAGATCTACAAATCGGCTTCCCGTGGCCAG 540
Db 376 AGAAGCTTCAACCTGCGGAGTTGCTGAGATCTACAAATCGGCTTCCCGTGGCCAG 317
OY 541 TTTTTCACAAATGTCAGAGGAGAGTGGCTGGGAGAGAAAGACTTGTATGAGCTTCT 600
Db 316 TTTTTCACAAATGTCAGAGGAGAGTGGCTGGGAGAGAAAGACTTGTATGAGCTTCT 257
OY 601 CCTTATTAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db 256 CCTTATTAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 197
OY 661 TTTTATTAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db 196 TTTTATTAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 137
OY 721 TTTTATTAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
Db 136 TTTTATTAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 77
OY 781 TGTGATGCGAT 840
Db 76 TGTGATGCGAT 17
OY 841 AAAAAAAAAAATCTGAG 856
Db 16 AAAAAAAAAAATCTGAG 1

RESULT 2

US-09-060-726A-1

Sequence 1, Application US/09060726A
Patent No. 6225350
GENERAL INFORMATION:
APPLICANT: Weigel, Detlef
APPLICANT: Salk Institute
TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY
TITLE OF INVENTION: MODIFIED PLANTS HAVING MODULATED FLOWER DEVELOPMENT
FILE REFERENCE: SALKINS. 026A
CURRENT APPLICATION NUMBER: US/09/060.726A
CURRENT FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 855
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: CDS
LOCATION: (63)...(590)
US-09-060-726A-1

Query Match 98.4%; Score 842.4; DB 4; Length 855;

Best Local Similarity 99.8%; Pred. No. 1.2e-213; Mismatches 1; Indels 1; Gaps 1;

Matches 854; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
OY 1 TCTAGACTAGTATGATCCCGCGGCTGAGAAATTCAGACAGAGTTGTTCAAGATCAA 60
Db 1 TCTAGACTAGTATGATCCCGCGGCTGAGAAATTCAGACAGAGTTGTTCAAGATCAA 60
OY 61 AGATGCTATATAATTAAGAGACCTCTTAATAGTACAGAGAGTTGTTGAGAGCTTTG 120
Db 61 AGATGCTATATAATTAAGAGACCTCTTAATAGTACAGAGAGTTGTTGAGAGCTTTG 120
OY 121 ATCGGTTAATGATCATCTTAAGGTTACTTATGCGCAAGAGAGGATGATATG 180
Db 121 ATCGGTTAATGATCATCTTAAGGTTACTTATGCGCAAGAGAGGATGATATG 180

OY 181 GCTTGATCTAAGGCGCTTCTCAGGTTCAAAACAGCCAGAGTGGATGTTGGAGAG 240
Db 181 GCTTGATCTAAGGCGCTTCTCAGGTTCAAAACAGCCAGAGTGGATGTTGGAGAG 240
OY 241 ACCTCAGAACTTCTATCTTGTGTTATGTTGATGATGATGATGATGATGATGATGAT 300
Db 241 ACCTCAGAACTTCTATCTTGTGTTATGTTGATGATGATGATGATGATGATGATGAT 300
OY 301 CTCACCTCGAGAAATATCCCAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 360
Db 301 CTCACCTCGAGAAATATCTCCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 360
OY 361 CCTTGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Db 361 CCTTGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
OY 421 TCGTGTATATATGTTTTCACAGCTTGGCAGCAACAGTATGACACAGGTTGGCGCC 480
Db 421 TCGTGTATATATGTTTTCACAGCTTGGCAGCAACAGTATGACACAGGTTGGCGCC 480
OY 481 AGAAGCTTCAACCTGCGGAGTTGCTGAGATCTACAAATCGGCTTCCCGTGGCCAG 540
Db 481 AGAAGCTTCAACCTGCGGAGTTGCTGAGATCTACAAATCGGCTTCCCGTGGCCAG 540
OY 541 TTTTTCACAAATGTCAGAGGAGAGTGGCTGGGAGAGAAAGACTTATGATGCTTCT 600
Db 541 TTTTTCACAAATGTCAGAGGAGAGTGGCTGGGAGAGAAAGACTTATGATGCTTCT 600
OY 601 CCTTATTAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db 601 CCTTATTAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 659
OY 661 TTTTATTAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db 661 TTTTATTAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 719
OY 721 TTTTATTAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
Db 721 TTTTATTAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 779
OY 781 TGTGATGCGAT 840
Db 781 TGTGATGCGAT 839
OY 841 AAAAAAAAAAATCTGAG 856
Db 841 AAAAAAAAAAATCTGAG 855

RESULT 3

US-07-644-372-1

Sequence 1, Application US/07644372

Patent No. 541609
GENERAL INFORMATION:
APPLICANT: Lazzeri, Mario E.
APPLICANT: Nutman, Thomas B.
APPLICANT: Weiss, Niklaus
TITLE OF INVENTION: A DNA SEGMENT ENCODING A SPECIFIC
TITLE OF INVENTION: IMMUNODIAGNOSTIC ANTIGEN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1615 L. Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/644,372
FILING DATE: 19910123
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)861-3000
TELEFAX: (202)822-0944
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 822 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 52..507
US-07-644-372-1
```

```

Query Match      8.4%; Score 71.8; DB 1; Length 822;
Best local Similarity 51.3%; Pred. No. 5.8e-10;
Matches 217; Conservative 0; Mismatches 202; Indels 4; Gaps 2;
```

```

QY 145 TAAAGTTACTTATGGCCAAAGAGAGTACTAATGCTTGAATCTAAGCCCTTCTCAGG 204
    |||||
DB 215 TCAATGTTAGTACAATAATCTCAGGTAATCTGGGCATTAAGCCGACGAGG 274

QY 205 TTCAAAACAAAGCCCAAGTTGAGATTGTTGAGAAAGCTCAGAACTTCTATCTTTGG 264
    |||||
DB 275 TAAAGATATGCGCGCAAAAGATATCATGAGATCGGAACCTGAGCCTTATATACGCTCG 334

QY 265 TTATGGTGCATCCAGATGTTCCAAAGTCTTCAACCCCTCACTCCGAAATATCTCATT 324
    |||||
DB 335 TTATGATGATCCCGAGCAGCACCATCTCGAAAAAACCCTGATTCAGAGATGCGACCAT 394

QY 325 GGTGGTGCATGATATCCCTGCTCAACAATG-GAACAACCTTGGCAATGAGATTGTGT 383
    |||||
DB 395 GGTGATTAATTAATTAATTTCTGGACAAATGTTAGACAGTGCACAGTCTTATCTGATAT 454

QY 384 TAGGAAATCCAGTCCCACTGCAAGATTCATGCTGCTGTTTATATTGTTTCGACAG 443
    |||||
DB 455 GATGACAGTCCAGAAAGGACAGAGACCTTCATGTTATGTTGTTTATTAACAA 514

QY 444 CTTGGCAGCAAGAGTATGTCACACGAGGTG---GCGCCAGAACTTCAACACTCGCGAG 500
    |||||
DB 515 CCTGGAAGTATCAGCGATCTCAACATGCGGGAATGCGGAAATTTCAAAAGTTATGAT 574

QY 501 TTGCTGAGATCTACAAATCTCGCCCTTCCGTCGCGCAGTTTCTTCAATTTGTCAAGG 560
    |||||
DB 575 TTGCAAAACAAACATCACTTGGAATAATCCAGTTGCGGAAACTTCTTCCAGGCTAAACAT 634

QY 561 GAG 563
    |||
DB 635 GAG 637
```

RESULT 4

```

US-08-467-948A-3/C
Sequence 3, Application US/08467948A
Patent No. 5996164
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR2
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
```

```

CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2185 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 884..2062
US-08-467-948A-3
```

```

Query Match      5.5%; Score 47; DB 2; Length 2185;
Best local Similarity 90.9%; Pred. No. 0.003;
Matches 50; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```

QY 1 TCTGAACATGATGATCCCGGCGCTGCAGGAATTCAGCAGAGTTGTTCAAG 55
    |||||
DB 2072 TCTGAACATGATGATCCCGGCGCTGCAGGAATTCAGCAGAGTTGTTGTTGAG 2018
```

RESULT 5

```

US-08-467-947A-3/C
Sequence 3, Application US/08467947A
Patent No. 6090575
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR1
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,947A
```

FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2185 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 884..2062
US-08-467-947A-3

Query Match
Best Local Similarity 5.5%; Score 47; DB 3; Length 2185;
Matches 50; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCTAGACTAGTGGATCCCGGCTGCAGGAATTCAGACGAGTTTCTTCAAG 55
DB 2072 TCTAGACTAGTGGATCCCGGCTGCAGGAATTCAGACGAGTTGTTGTTGAG 2018

RESULT 6
US-08-485-455D-60
Sequence 60, Application US/08485455D
Patent No. 5712143
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Slegler, Gary L.
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
NUMBER OF SEQUENCES: 79
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US/08/485,455D
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C1-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..234
US-08-485-455D-60

Query Match
Best Local Similarity 5.5%; Score 46.8; DB 1; Length 234;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 TCTAGACTAGTGGATCCCGGCTGCAGGAATTCAGACGAGTTTCTTCAAGTCAA 60
DB 48 TCTAGACTAGTGGATCCCGGCTGCAGGAATTCAGACGAGTTGTTGATTGA 107

QY 61 ACATGCTAATAATATAAGAGA 82
DB 108 GCGCGTCTCATCTTACAGATA 129

RESULT 7
US-08-482-130C-60
Sequence 60, Application US/08482130C
Patent No. 5962257
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Slegler, Gary L.
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
NUMBER OF SEQUENCES: 79
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US/08/482,130C
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..234
US-08-482-130C-60

Query Match
Best Local Similarity 5.5%; Score 46.8; DB 2; Length 234;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

OY	1	TCTGAACTACTGGATATCCCCGGGGCTGAGAAATTCAGCAGAGTTGTTCAGACAA	60
Db	48	TCTGAACTACTGGATATCCCCGGGGCTGAGAAATTCGACAGAGCTTTGTGGATGTA	107
OY	61	AGATGCTCTATTAATATTAAGGA	82
Db	108	GGCGCTCTCATCTTACCAAGATA	129

RESULT 8
US-08-484-211C-60.
; Sequence 60, Application US/08484211C

1 GENERAL INFORMATION:
2 APPLICANT: Grieve, Robert B.
3 APPLICANT: Rushlow, Keith E.
4 APPLICANT: Wu Hunter, Shirley
5 APPLICANT: Frank, Glenn R.
6 APPLICANT: Stiegler, Gary L.
7 TITLE OF INVENTION: PLEA PROTEASE PROTEINS, NUCLEIC ACID
8 TITLE OF INVENTION: MOLECULES, AND USES THEREOF
9
10 NUMBER OF SEQUENCES: 79
11
12 CORRESPONDENCE ADDRESSES:

```

; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80203
;

```

```

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
;

```

APPLICATION NUMBER: US/08/484,211C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary T

REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223

```

SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

```

```

; MOLECULE TYPE: CDN
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..234

```

Query Match	5.5%	Score 46.8;	DB 2;	Length 234;
Best Local Similarity	73.2%;	Pred. No. 0.0015;		
Matches	60;	Conservative	0;	Mismatches 22;
				Indels

1 TCTAACATACGATCCCCGGGCTGACGGAATTCACAGAGGTGTTCACAGATCAA 80
 48 TCTGAACCTATGTGATCCCCGGGGCTGCAGGAATTCGGCACGACGCTTTGGTTGGATTGA 107
 61 AGATGCTATATAATATATAGAGA 82

```

Db      108 GCGCGTTCATCTTCAAGATA 129
RESULT 9

```

US-08-906-769-60
; Sequence 60, Application US/08906769

Patent No. 6077687
GENERAL INFORMATION:
ADDITANT, Cr400

APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J.
APPLICANT: Silver, Gary

TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
 TITLE OF INVENTION: MOLECULES AND USES THEREOF
 NUMBER OF SEQUENCES: 190
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sheridan Ross & McIntosh

CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80203

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
Copyright 1990, PatentIn, Inc.

APPLICATION NUMBER: 05/08/906,765
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,072

FILING DATE: 24 APR 1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Connell, Gary J.
 REGISTRATION NUMBER: 32,020
 REFERENCE/DOCKET NUMBER: 2618-25-C3

TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE

NAME/KEY:	CDS
LOCATION:	1..234
S-08-906-769-60	
Query Match	

Seq. ID	Accession	Length	Score	E-value	Identical	Similarity	Pos. Local	Pos. Global	Matches	Mismatches	Conservative	Indels	Gaps
1	TC7AGAACCTAGTGGATCCCCCGGCGTCGACAGAAATTCAGCACGAGTTTGTTCAGATCAA	60	100	0.000000	100	100	100	100	60	0	22	0	0

61 AGATGCTATTAATATATAGACA 82
 |||| | |||| |
 108 GCGCGTCTCATCTTACAAATATA 129

RESULT 10
S-08-906-616-60
Sequence 60, Application US/08906616

APPLICANT:	Rushlow, Keith E.
APPLICANT:	Wu Hunter, Shirle
APPLICANT:	Frank, Glenn R.
APPLICANT:	Stiegler, Gary

APPLICANT: Gaines, Patrick J.
APPLICANT: Silver, Gary
TITLE OF INVENTION: FLEA AMINOPEPTIDASE PROTEINS AND USES THEREOF
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,616
FILING DATE: 05-AUG-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..234
US-08-906-616-60

Query Match
Best Local Similarity 5.5%; Score 46.8; DB 3; Length 234;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 TCTAGACCTAGTGGATCCCGGGCTGCAGGATTCAGCAGCGAGTTGTTCAAGATCAA 60
DB 48 TCTAGACCTAGTGGATCCCGGGCTGCAGGATTCAGCAGCGAGTTGTTGATTTGA 107
QY 61 AGATGCTCTAATATATAAGAGA 82
DB 108 GCGCGTCTCATCTTACAGAGATA 129

RESULT 11
US-08-817-795-60
Sequence 60, Application US/08817795
Patent No. 6139840
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Frank, Glenn R.
APPLICANT: Heath, Andrew W.
APPLICANT: Yamaka, Miles Yamataka
APPLICANT: Afstien, Ann
APPLICANT: Dale, Beverly
APPLICANT: Stiegler, Gary
TITLE OF INVENTION: USE OF PROTEASE INHIBITORS AND
TITLE OF INVENTION: PROTEASE VACCINES TO PROTECT ANIMALS FROM FLEA
TITLE OF INVENTION: INFESTATION, AND FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES, AND USES THEREOF
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh

STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,795
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14442
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gary J. Connell
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..234
US-08-817-795-60

Query Match
Best Local Similarity 5.5%; Score 46.8; DB 3; Length 234;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 TCTAGACCTAGTGGATCCCGGGCTGCAGGATTCAGCAGCGAGTTGTTCAAGATCAA 60
DB 48 TCTAGACCTAGTGGATCCCGGGCTGCAGGATTCAGCAGCGAGTTGTTGATTTGA 107
QY 61 AGATGCTCTAATATATAAGAGA 82
DB 108 GCGCGTCTCATCTTACAGAGATA 129

RESULT 12
US-08-485-443B-60
Sequence 60, Application US/08485443B
Patent No. 6146870
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary L.
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES AND USES THEREOF
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: SHERIDAN ROSS
STREET: 1700 LINCOLN ST., SUITE 3500
CITY: DENVER
STATE: CO
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,443B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary L.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C1-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303 863-9700
TELEFAX: 303 863-0223
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..234
US-08-485-443B-60

Query Match
Best Local Similarity 73.2%; Pred. No. 0.0015;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

OY 1 TCTAGACTAGTGGATCCCGGCTGCAGGAATTACACGAGGTTGTTCAAGATCAA 60
|||||
Db 48 TCTAGACTAGTGGATCCCGGCTGCAGGAATTACGACGAGGTTGTTGATTTGA 107

OY 61 AGATGCTATAATATTAAGAGA 82
|||||
Db 108 GCGGCTCTCATCTTACAGAGATA 129

RESULT 13
US-08-639-075A-60
Sequence 60, Application US/08639075A
Patent No. 6150125
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J.
APPLICANT: Silver, Gary
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/639,075A
FILING DATE: 24-APR-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..234
US-08-639-075A-60

Query Match
Best Local Similarity 73.2%; Pred. No. 0.0015;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

OY 1 TCTAGACTAGTGGATCCCGGCTGCAGGAATTACACGAGGTTGTTCAAGATCAA 60
|||||
Db 48 TCTAGACTAGTGGATCCCGGCTGCAGGAATTACGACGAGGTTGTTGATTTGA 107

OY 61 AGATGCTATAATATTAAGAGA 82
|||||
Db 108 GCGGCTCTCATCTTACAGAGATA 129

RESULT 14
US-09-012-431-60
Sequence 60, Application US/09012431
Patent No. 6180383
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J.
APPLICANT: Silver, Gary
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,431
FILING DATE: 23-Jan-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,075
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..234
SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-09-012-431-60

Query Match 5.5%; Score 46.8; DB 4; Length 234;
Best Local Similarity 73.2%; Pred. No. 0.0015;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 TCTAGAACTAGTGGATCCCGGGCTGCAGGAATTCAGCAGAGTTGTTCAAGATCAA 60
|||||
Db 48 TCTAGAACTAGTGGATCCCGGGCTGCAGGAATTCGCGCAGAGCGTTGTTGATTTGA 107
QY 61 AGATGCTATATAATATAGAGA 82
|||||
Db 108 GCGCGTCTCATCTTACAAAGATA 129

RESULT 15

US-09-012-692-60
Sequence 60, Application US/09012692
Patent No. 6214579

GENERAL INFORMATION:

APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J.
APPLICANT: Silver, Gary
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
NUMBER OF INVENTION: MOLECULES AND USES THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80203

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,692

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/639,075

FILING DATE: 24-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2

TELEPHONE: (303) 863-9700

TELEFAX: (303) 863-0223

INFORMATION FOR SEQ ID NO: 60:

SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..234

US-09-012-692-60

Query Match 5.5%; Score 46.8; DB 4; Length 234;
Best Local Similarity 73.2%; Pred. No. 0.0015;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 TCTAGAACTAGTGGATCCCGGGCTGCAGGAATTCAGCAGAGTTGTTCAAGATCAA 60
|||||
Db 48 TCTAGAACTAGTGGATCCCGGGCTGCAGGAATTCGCGCAGAGCGTTGTTGATTTGA 107
QY 61 AGATGCTATATAATATAGAGA 82
|||||
Db 108 GCGCGTCTCATCTTACAAAGATA 129

Search completed: May 1, 2003, 21:56:13
Job time : 65 secs

QY 181 GCTTGGATCTAAGCCCTTCTCAGTTCAAAACCAAGCAGAGTTGAGATTGTGGAGAA 240
|||||
Db 181 GCTTGGATCTAAGCCCTTCTCAGTTCAAAACCAAGCAGAGTTGAGATTGTGGAGAA 240
QY 241 ACCTGAGAACTTCTTACTTTGGTATATGTGTGATCCAGATGTTCCAAAGTCTGACAA 300
|||||
Db 241 ACCTGAGAACTTCTTACTTTGGTATATGTGTGATCCAGATGTTCCAAAGTCTGACAA 300
QY 301 CTCACCTCCGAGAAATATCTCATTGGTTGGTGTGATATCCCTGTACAACTGSAACAA 360
|||||
Db 301 CTCACCTCCGAGAAATATCTCATTGGTTGGTGTGATATCCCTGTGTACAACTGSAACAA 360
QY 361 CCTTTGGCAATGAGATGTGTGTACGAAATCCAAAGTCCCACTGCAAGAAATTCATG 420
|||||
Db 361 CCTTTGGCAATGAGATGTGTGTACGAAATCCAAAGTCCCACTGCAAGAAATTCATG 420
QY 421 TCGTGTATATTTGTTTCCAGACCTTGGCAGGCAAAACAGTATGCAACAGGTTGGCC 480
|||||
Db 421 TCGTGTATATTTGTTTCCAGACCTTGGCAGGCAAAACAGTATGCAACAGGTTGGCC 480
QY 481 AGAAGCTTCAACACTCGAGATTGCTGAGATCTACAATCTCGGCTTCCCGTGGCCGAG 540
|||||
Db 481 AGAAGCTTCAACACTCGAGATTGCTGAGATCTACAATCTCGGCTTCCCGTGGCCGAG 540
QY 541 TTTTCTCAATTTGTCTAGAGAGAGAGTGGCTGGCAGAGAAAGACTTTAGAGGCTTCT 600
|||||
Db 541 TTTTCTCAATTTGTCTAGAGAGAGAGTGGCTGGCAGAGAAAGACTTTAGAGGCTTCT 600
QY 601 CCTTTTAAACAATTTGATTTGATCTGATGATGATTTATGATTTATGATTTTAA 660
|||||
Db 601 CCTTTTAAACAATTTGATTTGATCTGATGATGATTTATGATTTATGATTTTAA 660
QY 661 TTTAATTAACCAATTTATGATAGAGTAAGCAAGGATGATGATGATTTATGATTTTAA 720
|||||
Db 661 TTTAATTAACCAATTTATGATAGAGTAAGCAAGGATGATGATGATTTATGATTTTAA 720
QY 721 TATAAGTGTATATAAATGAGAGGGGAGGAGAAATGAGAGTGTCTTACTTATATAG 780
|||||
Db 721 TATAAGTGTATATAAATGAGAGGGGAGGAGAAATGAGAGTGTCTTACTTATATAG 780
QY 781 TGTGATGCGATATTTATATATCTACATGAATGAAGTGTATATTTATATATATAT 840
|||||
Db 781 TGTGATGCGATATTTATATATCTACATGAATGAAGTGTATATTTATATATATAT 840
QY 841 AAAAAAAAAAATCTGAG 856
|||||
Db 841 AAAAAAAAAAATCTGAG 856

RESULT 2
US-09-291-809C-3/C
; Sequence 3, Application US/09291809C
; Patent No. US20010049831A1
; GENERAL INFORMATION:
; APPLICANT: Delfel weigel
; APPLICANT: Salk Institute
; TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY
; FILE REFERENCE: SALKINS 026CPI
; CURRENT APPLICATION NUMBER: US/09/291,809C
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: PCT/US99/08151
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 09/060,726
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 856
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-291-809C-3

Query Match 100.0%; Score 856; DB 10; Length 856;
Best Local Similarity 100.0%; Pred. No. 9e-206;
Matches 856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTAGAACTAGTGGATCCCCGGGGTGCAGGAATTCAGCAGAGTTTGTTCAGATCAA 60
|||||
Db 856 TCTAGAACTAGTGGATCCCCGGGGTGCAGGAATTCAGCAGAGTTTGTTCAGATCAA 60
QY 61 AGATGCTATTAATATTAAGAGACCTCTTATTAAGCAGAGTTTGGAGACTCTTG 120
|||||
Db 796 AGATGCTATTAATATTAAGAGACCTCTTATTAAGCAGAGTTTGGAGACTCTTG 120
QY 121 ATCCGTTTATATGATCAATCTCTAAAGTTTACTTATGCGCAAGAGAGTACTAATG 180
|||||
Db 736 ATCCGTTTATATGATCAATCTCTAAAGTTTACTTATGCGCAAGAGAGTACTAATG 180
QY 181 GCTTGGATCTAAGCCCTTCTCAGGTTCAAAACAGCCAGAGTTGATGTTGGAGAA 240
|||||
Db 676 GCTTGGATCTAAGCCCTTCTCAGGTTCAAAACAGCCAGAGTTGATGTTGGAGAA 240
QY 241 ACCTCAGAACTCTTACTTGTGTTATGATGATGATGATGATGATGATGATGATGAT 300
|||||
Db 616 ACCTCAGAACTCTTACTTGTGTTATGATGATGATGATGATGATGATGATGATGAT 300
QY 301 CTCACCTCCGAGAAATATCTCATTGGTTGGTGTGATGATGATGATGATGATGATGAT 360
|||||
Db 556 CTCACCTCCGAGAAATATCTCATTGGTTGGTGTGATGATGATGATGATGATGATGAT 360
QY 361 CCTTTGGCAATGAGATGTGTGTACGAAATCCAAAGTCCCACTGCAAGAAATTCATG 420
|||||
Db 496 CCTTTGGCAATGAGATGTGTGTACGAAATCCAAAGTCCCACTGCAAGAAATTCATG 420
QY 421 TCGTGTATATTTGTTTCCAGACCTTGGCAGGCAAAACAGTATGCAACAGGTTGGCC 480
|||||
Db 436 TCGTGTATATTTGTTTCCAGACCTTGGCAGGCAAAACAGTATGCAACAGGTTGGCC 480
QY 481 AGAAGCTTCAACACTCGAGATTGCTGAGATCTACAATCTCGGCTTCCCGTGGCCGAG 540
|||||
Db 376 AGAAGCTTCAACACTCGAGATTGCTGAGATCTACAATCTCGGCTTCCCGTGGCCGAG 540
QY 541 TTTTCTCAATTTGTCTAGAGAGAGTGGCTGGCAGAGAAAGACTTTAGAGGCTTCT 600
|||||
Db 316 TTTTCTCAATTTGTCTAGAGAGAGTGGCTGGCAGAGAAAGACTTTAGAGGCTTCT 600
QY 601 CCTTTTAAACAATTTGATTTGATCTGATGATGATTTATGATTTATGATTTTAA 660
|||||
Db 256 CCTTTTAAACAATTTGATTTGATCTGATGATGATTTATGATTTATGATTTTAA 660
QY 661 TTTAATTAACCAATTTATGATAGAGTAAGCAAGGATGATGATGATTTATGATTTTAA 720
|||||
Db 196 TTTAATTAACCAATTTATGATAGAGTAAGCAAGGATGATGATGATTTATGATTTTAA 720
QY 721 TATAAGTGTATATAAATGAGAGGGGAGGAGAAATGAGAGTGTCTTACTTATATAG 780
|||||
Db 136 TATAAGTGTATATAAATGAGAGGGGAGGAGAAATGAGAGTGTCTTACTTATATAG 780
QY 781 TGTGATGCGATATTTATATCTACATGAATGAAGTGTATATTTATATATATATAT 840
|||||
Db 76 TGTGATGCGATATTTATATCTACATGAATGAAGTGTATATTTATATATATATAT 840
QY 841 AAAAAAAAAAATCTGAG 856
|||||
Db 16 AAAAAAAAAAATCTGAG 1

RESULT 3
US-09-845-849-1
; Sequence 1, Application US/09845849
; Patent No. US20020029395A1
; GENERAL INFORMATION:
; APPLICANT: THE SALK INSTITUTE FOR BIOLOGICAL STUDIES
; APPLICANT: WEIGEL, Delfel

```

; APPLICANT: KARDALISKY, Igor
; TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY
; FILE REFERENCE: SALKINS-026DVI
; CURRENT APPLICATION NUMBER: US/09/845,849
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 09/060,726
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 856
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-845-849-1

Query Match      100.0%; Score 856; DB 10; Length 856;
Best Local Similarity 100.0%; Pred. No. 9e-206;
Matches 856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTAGAACTAGTGGATCCCCGGGCTCCAGGAATTCAGCAGAGGTTTGTCAAGATCAA 60
    |||||||
DB 1 TCTAGAACTAGTGGATCCCCGGGCTCCAGGAATTCAGCAGAGGTTTGTCAAGATCAA 60

QY 61 AGATGCTATATAATATAAGAGACCCCTTATAGTACAGAGGTTGGAGACGTTCTTG 120
    |||||||
DB 61 AGATGCTATATAATATAAGAGACCCCTTATAGTACAGAGGTTGGAGACGTTCTTG 120

QY 121 ATCCGTTTAATAGATCAATCACTCTAAGGTTACTTATGGCCAAAGAGAGTGAATATG 180
    |||||||
DB 121 ATCCGTTTAATAGATCAATCACTCTAAGGTTACTTATGGCCAAAGAGAGTGAATATG 180

QY 181 GCTTGAGATCAAGCCCTTCTCAGGTTCAAAACAAGCCAGAGTTGAGATTGGAGAGAG 240
    |||||||
DB 181 GCTTGAGATCAAGCCCTTCTCAGGTTCAAAACAAGCCAGAGTTGAGATTGGAGAGAG 240

QY 241 ACCTCAGAGACTCTATCTAGTTGGTATGAGTATCCAGATGTTCCAAAGTCTTCAAGC 300
    |||||||
DB 241 ACCTCAGAGACTCTATCTAGTTGGTATGAGTATCCAGATGTTCCAAAGTCTTCAAGC 300

QY 301 CTCACCTCCGAGAAATATCTCCANTGGTTGGTACTGATATCCCTGATCAACATGGAACAA 360
    |||||||
DB 301 CTCACCTCCGAGAAATATCTCCANTGGTTGGTACTGATATCCCTGATCAACATGGAACAA 360

QY 361 CCTTGGCAATGAGATGTGTGTACGAAATCCAAAGTCCACAGCAGGAATTTATGCTG 420
    |||||||
DB 361 CCTTGGCAATGAGATGTGTGTACGAAATCCAAAGTCCACAGCAGGAATTTATGCTG 420

QY 421 TCGGTTTATATGTTTTCGACAGCTTGCGAGCAAAACAGTGTATGACACAGGATGCGCC 480
    |||||||
DB 421 TCGGTTTATATGTTTTCGACAGCTTGCGAGCAAAACAGTGTATGACACAGGATGCGCC 480

QY 481 AGAAGCTTCAACACTCGGAGTTTGCTGAGATCTTCAATCTCCGCTCCGCGCCAG 540
    |||||||
DB 481 AGAAGCTTCAACACTCGGAGTTTGCTGAGATCTTCAATCTCCGCTCCGCGCCAG 540

QY 541 TTTTCTCAATGTCACAGAGAGAGTGGCTGCGAGCAAGAACTTTAGTGGCTTCTT 600
    |||||||
DB 541 TTTTCTCAATGTCACAGAGAGAGTGGCTGCGAGCAAGAACTTTAGTGGCTTCTT 600

QY 601 CCTTATTAACCAATTTGATATGCTATCTGATGAGATTTTATGATCTATATGTTTAA 660
    |||||||
DB 601 CCTTATTAACCAATTTGATATGCTATCTGATGAGATTTTATGATCTATATGTTTAA 660

QY 661 TTTTATTAACCAATTTGATATGCTATCTGATGAGATTTTATGATCTATATGTTTAA 720
    |||||||
DB 661 TTTTATTAACCAATTTGATATGCTATCTGATGAGATTTTATGATCTATATGTTTAA 720

QY 721 TATAGAGTGTATATAAAGAGAGAGGAGGAGAAATGAGAGTGTATTAATATAGTGTG 780
    |||||||
DB 721 TATAGAGTGTATATAAAGAGAGAGGAGGAGAAATGAGAGTGTATTAATATAGTGTG 780

QY 781 TGTGATCGATATATATATTAATCTACATGAATGAAGTGTATATATATATATATATAT 840
    |||||||
```

```

|||||
DB 781 TGTATCGGAATATATATATATCTACATGAATGAAGTGTATATATATATATATATAT 840

QY 841 AAAAAAAAAAACTCGAG 856
    |||||||
DB 841 AAAAAAAAAAACTCGAG 856

RESULT 4
US-09-845-849-3/c
; Sequence 3, Application US/09845849
; Patent No. US20020029395A1
; GENERAL INFORMATION:
; APPLICANT: THE SALK INSTITUTE FOR BIOLOGICAL STUDIES
; APPLICANT: WEGEL, Detlef
; APPLICANT: KARDALISKY, Igor
; TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY
; FILE REFERENCE: SALKINS-026DVI
; CURRENT APPLICATION NUMBER: US/09/845,849
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 09/060,726
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 856
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-845-849-3

Query Match      100.0%; Score 856; DB 10; Length 856;
Best Local Similarity 100.0%; Pred. No. 9e-206;
Matches 856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTAGAACTAGTGGATCCCCGGGCTCCAGGAATTCAGCAGAGGTTTGTCAAGATCAA 60
    |||||||
DB 856 TCTAGAACTAGTGGATCCCCGGGCTCCAGGAATTCAGCAGAGGTTTGTCAAGATCAA 60

QY 61 AGATGCTATATAATATAAGAGACCCCTTATAGTACAGAGGTTGGAGACGTTCTTG 120
    |||||||
DB 61 AGATGCTATATAATATAAGAGACCCCTTATAGTACAGAGGTTGGAGACGTTCTTG 120

QY 121 ATCCGTTTAATAGATCAATCACTCTAAGGTTACTTATGGCCAAAGAGAGTGAATATG 180
    |||||||
DB 121 ATCCGTTTAATAGATCAATCACTCTAAGGTTACTTATGGCCAAAGAGAGTGAATATG 180

QY 181 GCTTGAGATCAAGCCCTTCTCAGGTTCAAAACAAGCCAGAGTTGAGATTGGAGAGAG 240
    |||||||
DB 181 GCTTGAGATCAAGCCCTTCTCAGGTTCAAAACAAGCCAGAGTTGAGATTGGAGAGAG 240

QY 241 ACCTCAGAGACTCTATCTAGTTGGTATGAGTATCCAGATGTTCCAAAGTCTTCAAGC 300
    |||||||
DB 241 ACCTCAGAGACTCTATCTAGTTGGTATGAGTATCCAGATGTTCCAAAGTCTTCAAGC 300

QY 301 CTCACCTCCGAGAAATATCTCCANTGGTTGGTACTGATATCCCTGATCAACATGGAACAA 360
    |||||||
DB 301 CTCACCTCCGAGAAATATCTCCANTGGTTGGTACTGATATCCCTGATCAACATGGAACAA 360

QY 361 CCTTGGCAATGAGATGTGTGTACGAAATCCAAAGTCCACAGCAGGAATTTATGCTG 420
    |||||||
DB 361 CCTTGGCAATGAGATGTGTGTACGAAATCCAAAGTCCACAGCAGGAATTTATGCTG 420

QY 421 TCGGTTTATATGTTTTCGACAGCTTGCGAGCAAAACAGTGTATGACACAGGATGCGCC 480
    |||||||
DB 421 TCGGTTTATATGTTTTCGACAGCTTGCGAGCAAAACAGTGTATGACACAGGATGCGCC 480

QY 481 AGAAGCTTCAACACTCGGAGTTTGCTGAGATCTTCAATCTCCGCTCCGCGCCAG 540
    |||||||
DB 481 AGAAGCTTCAACACTCGGAGTTTGCTGAGATCTTCAATCTCCGCTCCGCGCCAG 540

QY 541 TTTTCTCAATGTCACAGAGAGAGTGGCTGCGAGCAAGAACTTTAGTGGCTTCTT 600
    |||||||
```

Db 316 TTTTACAAATGTCAGAGAGAGAGTGGCTCCGAGAGAAAGACCTTAGATGCTTCTT 257
Qy 601 CCTTATTAACCAATGATATGCACTCTGATGAGATTTATGACCTATAGATTTTAA 660
Db 256 CCTTTATTAACCAATGATATGCACTCTGATGAGATTTATGACCTATAGATTTTAA 197
Qy 661 TTTTAAACCAATTTTATGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db 196 TTTTAAACCAATTTTATGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 137
Qy 721 TTTTAAACCAATTTTATGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Db 136 TTTTAAACCAATTTTATGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 77
Qy 781 TTTTAAACCAATTTTATGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Db 76 TTTTAAACCAATTTTATGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 17
Qy 841 AAAAAAAAAAATCTGAG 856
Db 16 AAAAAAAAAAATCTGAG 1

RESULT 5

US-09-938-842A-2635
Sequence 2635, Application US/0993842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: S001300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2635
LENGTH: 528
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-2635

Query Match 44.1% Score 377.6; DB 9; Length 528;
Best Local Similarity 82.2%; Pred. No. 2.1e-85;
Matches 434; Conservative 0; Mismatches 94; Indels 0; Gaps 0;
Qy 63 AGCTGATTAATAAG 122
Db 1 AGCTGATTAATAAG 60
Qy 123 CGGTTAATGATCAATCACTCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 182
Db 61 CCTTTCAG 120
Qy 183 TTGATCTAAG 242
Db 121 TTGATCTAAG 180
Qy 243 CTCAG 302
Db 181 TTCAAG 240
Qy 303 CACCTCGAG 362
Db 241 CACCAAG 300

Qy 363 TTGSCAATGAGATGTTGTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 422
Db 301 TTGSCAATGAGATGTTGTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Qy 423 GGTGTTATTTGTTGAG 482
Db 361 GGTGTTATTTGTTGAG 420
Qy 483 AACTTCAG 542
Db 421 CAGTTCAAG 480
Qy 543 TTCTCAATTTGTCAG 590
Db 481 TACTCAATTTGTCAG 528

RESULT 6

US-09-938-842A-1501
Sequence 1501, Application US/0993842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: S001300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1501
LENGTH: 534
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-1501

Query Match 20.7% Score 176.8; DB 9; Length 534;
Best Local Similarity 60.6%; Pred. No. 7.8e-35;
Matches 308; Conservative 0; Mismatches 197; Indels 3; Gaps 1;
Qy 60 AAGATGCTAATAATAAG 119
Db 7 AAGATGCGAAG 66
Qy 120 GATCGTTAATAAGATCAATCACTCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 179
Db 67 GATCGTTAATAAGATCAATCACTCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 126
Qy 180 GCGTTGATCTAAG 239
Db 127 GCGCATAG 186
Qy 240 GACCTCAG 299
Db 187 GATCTCAG 246
Qy 300 CCTCAG 359
Db 247 CCTTCTAAG 306
Qy 360 ACCTTGGAG 419
Db 307 ACCTTGGAG 366

1 TCTAGACTAGTGGATCCCCGGGCTGCAGCAATTACAGCAGAGGTTTGTTC AAGATCAA 60

Db 76 TCTAGACTAGTGCATCCCGGCTGCAGGATTCGGCAGAGTTTATTATTATTTTA 135
 QY 61 AGATGCTCAT 70
 Db 136 TGGGCTTTT 145

RESULT 10
 US-10-074-095-248/c
 ; Sequence 248, Application US/10074095
 ; Publication No. US20030077704A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PC008C1
 ; CURRENT APPLICATION NUMBER: US/10/074,095
 ; CURRENT FILING DATE: 2002-02-14
 ; PRIOR APPLICATION NUMBER: 09/764,860
 ; PRIOR FILING DATE: 2001-01-17
 ; PRIOR APPLICATION NUMBER: 60/179,065
 ; PRIOR FILING DATE: 2000-01-31
 ; PRIOR APPLICATION NUMBER: 60/180,628
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: 60/214,886
 ; PRIOR FILING DATE: 2000-06-28
 ; PRIOR APPLICATION NUMBER: 60/217,487
 ; PRIOR FILING DATE: 2000-07-11
 ; PRIOR APPLICATION NUMBER: 60/225,758
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/220,963
 ; PRIOR FILING DATE: 2000-07-26
 ; PRIOR APPLICATION NUMBER: 60/217,496
 ; PRIOR FILING DATE: 2000-07-11
 ; PRIOR APPLICATION NUMBER: 60/225,447
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/218,290
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: 60/225,757
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/226,868
 ; PRIOR FILING DATE: 2000-08-22
 ; PRIOR APPLICATION NUMBER: 60/216,647
 ; PRIOR FILING DATE: 2000-07-07
 ; PRIOR APPLICATION NUMBER: 60/225,267
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/216,880
 ; PRIOR FILING DATE: 2000-07-07
 ; PRIOR APPLICATION NUMBER: 60/225,270
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/251,869
 ; PRIOR FILING DATE: 2000-12-08
 ; PRIOR APPLICATION NUMBER: 60/235,834
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/234,274
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: 60/234,223
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: 60/228,924
 ; PRIOR FILING DATE: 2000-08-30
 ; PRIOR APPLICATION NUMBER: 60/224,518
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/236,369
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: 60/224,519
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/220,964
 ; PRIOR FILING DATE: 2000-07-26
 ; PRIOR APPLICATION NUMBER: 60/241,809
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/249,299
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/236,327
 ; PRIOR FILING DATE: 2000-09-29

; PRIOR APPLICATION NUMBER: 60/241,785
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/244,617
 ; PRIOR FILING DATE: 2000-11-01
 ; PRIOR APPLICATION NUMBER: 60/225,268
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/236,368
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: 60/251,856
 ; PRIOR FILING DATE: 2000-12-08
 ; PRIOR APPLICATION NUMBER: 60/251,868
 ; PRIOR FILING DATE: 2000-12-08
 ; PRIOR APPLICATION NUMBER: 60/229,344
 ; PRIOR FILING DATE: 2000-09-01
 ; PRIOR APPLICATION NUMBER: 60/234,997
 ; PRIOR FILING DATE: 2000-09-25
 ; PRIOR APPLICATION NUMBER: 60/229,343
 ; PRIOR FILING DATE: 2000-09-01
 ; PRIOR APPLICATION NUMBER: 60/229,345
 ; PRIOR FILING DATE: 2000-09-01
 ; PRIOR APPLICATION NUMBER: 60/229,287
 ; PRIOR FILING DATE: 2000-09-01
 ; PRIOR APPLICATION NUMBER: 60/229,513
 ; PRIOR FILING DATE: 2000-09-05
 ; PRIOR APPLICATION NUMBER: 60/231,413
 ; PRIOR FILING DATE: 2000-09-08
 ; PRIOR APPLICATION NUMBER: 60/229,509
 ; PRIOR FILING DATE: 2000-09-05
 ; PRIOR APPLICATION NUMBER: 60/236,367
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: 60/237,039
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: 60/237,038
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: 60/236,370
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: 60/236,802
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: 60/237,037
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: 60/237,040
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: 60/240,960
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/239,935
 ; PRIOR FILING DATE: 2000-10-13
 ; PRIOR APPLICATION NUMBER: 60/239,937
 ; PRIOR FILING DATE: 2000-10-13
 ; PRIOR APPLICATION NUMBER: 60/241,787
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/246,474
 ; PRIOR FILING DATE: 2000-11-08
 ; PRIOR APPLICATION NUMBER: 60/246,532
 ; PRIOR FILING DATE: 2000-11-08
 ; PRIOR APPLICATION NUMBER: 60/249,216
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/249,210
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/226,681
 ; PRIOR FILING DATE: 2000-08-22
 ; PRIOR APPLICATION NUMBER: 60/225,759
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/225,213
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/227,182
 ; PRIOR FILING DATE: 2000-08-22
 ; PRIOR APPLICATION NUMBER: 60/225,214
 ; PRIOR FILING DATE: 2000-08-14
 ; PRIOR APPLICATION NUMBER: 60/235,836
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/230,438
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/215,135

```

: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: 60/225,266
: PRIOR FILING DATE: 2000-08-14
: PRIOR APPLICATION NUMBER: 60/249,218
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,208
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,213
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,212
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,207
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,245
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,244
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,217
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,211
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,215
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,264
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,214
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/249,297
: PRIOR FILING DATE: 2000-11-17
: PRIOR APPLICATION NUMBER: 60/232,400
: PRIOR FILING DATE: 2000-09-14
: PRIOR APPLICATION NUMBER: 60/231,242
: PRIOR FILING DATE: 2000-09-08
: PRIOR APPLICATION NUMBER: 60/232,081
: PRIOR FILING DATE: 2000-09-08
: PRIOR APPLICATION NUMBER: 60/232,080
: PRIOR FILING DATE: 2000-09-08
: PRIOR APPLICATION NUMBER: 60/231,414
: PRIOR FILING DATE: 2000-09-08
: PRIOR APPLICATION NUMBER: 60/231,244
: PRIOR FILING DATE: 2000-09-08
: PRIOR APPLICATION NUMBER: 60/233,064
: PRIOR FILING DATE: 2000-09-14
: PRIOR APPLICATION NUMBER: 60/233,063
: PRIOR FILING DATE: 2000-09-14
: PRIOR APPLICATION NUMBER: 60/232,397
: PRIOR FILING DATE: 2000-09-14
: PRIOR APPLICATION NUMBER: 60/232,399
: PRIOR FILING DATE: 2000-09-14
: PRIOR APPLICATION NUMBER: 60/232,401
: PRIOR FILING DATE: 2000-09-14
: PRIOR APPLICATION NUMBER: 60/241,808
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/241,826
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/241,786
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/241,221
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/246,475
: PRIOR FILING DATE: 2000-11-08
: PRIOR APPLICATION NUMBER: 60/231,243
: PRIOR FILING DATE: 2000-09-08

```

Query Match 5.6%; Score 48.2; DB 9; Length 367;
Best Local Similarity 76.6%; Pred. No. 0.016; Indels 0; Gaps 0;
Matches 59; Conservative 0; Mismatches 18;

```

QY 1 TCTAGAACTAGTGGATCCCGCGGCTGCAGAAATTCAGACGAGTTTCTCAAGATCAA 60
DB 305 TCTAGAACTAGTGGATCCCGCGGCTGCAGAAATTCAGACGAGTTTCTCAAGATCAA 246
QY 61 AGATGCTATATAATAATA 77

```

DB 245 TATCTTTTATGACACA 229

```

RESULT 11
US-09-764-860-248/c
: Sequence 248, Application US/09764860
: Patent No. US20020094953A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PC008
: CURRENT APPLICATION NUMBER: US/09/764,860
: PRIOR FILING DATE: 2001-01-17
: NUMBER OF SEQ ID NOS: 1198
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 248
: LENGTH: 367
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (345)
: OTHER INFORMATION: n equals a,t,g, or c
US-09-764-860-248

```

Query Match 5.6%; Score 48.2; DB 10; Length 367;
Best Local Similarity 76.6%; Pred. No. 0.016; Indels 0; Gaps 0;
Matches 59; Conservative 0; Mismatches 18;

```

QY 1 TCTAGAACTAGTGGATCCCGCGGCTGCAGAAATTCAGACGAGTTTCTCAAGATCAA 60
DB 305 TCTAGAACTAGTGGATCCCGCGGCTGCAGAAATTCAGACGAGTTTCTCAAGATCAA 246
QY 61 AGATGCTATATAATAATA 77
DB 245 TATCTTTTATGACACA 229

```

```

RESULT 12
US-09-925-300-816
: Sequence 816, Application US/09925300
: Patent No. US20020151681A1
: GENERAL INFORMATION:
: APPLICANT: Craig Rosen,
: APPLICANT: Steve Ruben,
: TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
: FILE REFERENCE: PA101
: CURRENT APPLICATION NUMBER: US/09/925,300
: PRIOR FILING DATE: 2001-08-10
: PRIOR APPLICATION NUMBER: PCT/US00/05988
: PRIOR FILING DATE: 2000-03-08
: PRIOR APPLICATION NUMBER: 60/124,270
: PRIOR FILING DATE: 1999-03-12
: NUMBER OF SEQ ID NOS: 1890
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 816
: LENGTH: 551
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (2)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (15)
: OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-816

```

Query Match 5.6%; Score 48; DB 10; Length 551;
Best Local Similarity 75.0%; Pred. No. 0.022; Indels 0; Gaps 0;
Matches 60; Conservative 0; Mismatches 20;

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using sw model

8903.503 Million cell updates/sec

Sequence: 1 ctcgagttttttttttt.....ggggaaccactagttctaga 856

Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 4109280

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

Maximum Match	100%
Post-processing:	Minimum Match 0%

Listing first 45 summaries

Database :

1:	GenEmb1.*
2:	gb_ba.*
3:	gb_hng.*
4:	gb_in.*
5:	gb_ov.*
6:	gb_pat.*
7:	gb_ph.*
8:	gb_pl.*
9:	gb_pro.*
10:	gb_ro.*
11:	gb_sts.*
12:	gb_sy.*
13:	gb_un.*
14:	gb_v1.*
15:	gb_ba.*
16:	em_fun.*
17:	em_hum.*
18:	em_in.*
19:	em_mu.*
20:	em_om.*
21:	em_ov.*
22:	em_ov.*
23:	em_pat.*
24:	em_ph.*
25:	em_pl.*
26:	em_ro.*
27:	em_sts.*
28:	em_un.*
29:	em_v1.*
30:	em_hng_hum.*
31:	em_hng_in.*
32:	em_hng_other.*
33:	em_hng_mu.*
34:	em_hng_pln.*
35:	em_hng_rod.*
36:	em_hng_mam.*
37:	em_hng_vit.*
38:	em_sy.*
39:	em_hngc_hum.*
40:	em_hngc_mu.*
41:	em_hngc_other

Pred. No. is the number of results predicted by chance to have a

Result No.	Score	Query Match	Length	DB	ID	Description
1	856	100.0	856	6	ARI48907	ARI48907 Sequence
2	842.4	98.4	855	6	ARI48906	ARI48906 Sequence
3	799.6	93.4	864	8	AB027504	AB027504 Arabidops
4	763.4	89.2	840	8	AY065378	AY065378 Arabidops
5	635.6	74.3	780	8	AB027505	AB027505 Arabidops
6	559	65.3	559	8	AY133813	AY133813 Arabidops
7	528	61.7	528	6	E38985	E38985 Method for
8	466	54.4	109560	8	F5114	AC001229 Sequence
9	465	54.3	2483	8	AF152096	AF152096 Arabidops
10	389.8	44.5	799	8	AB027506	AB027506 Arabidops
11	377.6	44.1	528	8	AF152907	AF152907 Arabidops
12	374.4	43.7	528	6	E38986	E38986 Method for
13	289.6	33.8	745	8	AB027456	AB027456 Citrus un
14	248.8	29.1	899	6	AX478001	AX478001 Sequence
15	248.4	29.0	847	8	AB052943	AB052943 Oryza sat
16	248	29.0	847	8	AB052944	AB052944 Oryza sat
17	239.8	28.0	1004	6	AX478049	AX478049 Sequence
18	238.6	27.9	866	8	AB062676	AB062676 Oryza sat
19	230.4	26.9	1191	6	AX478007	AX478007 Sequence
20	225.2	26.3	1078	6	AX477997	AX477997 Sequence
21	220.6	25.8	886	6	AX478033	AX478033 Sequence
22	196	22.9	836	6	AX478029	AX478029 Sequence
23	187	22.8	969	6	AX478027	AX478027 Sequence
24	185.8	21.7	492	6	AX477991	AX477991 Sequence
25	176.8	20.7	668	6	AE1530	AE1530 Sequence 4
26	176.8	20.7	668	8	ATU77674	ATU77674 Arabidopsis
27	175	20.4	837	6	AX478005	AX478005 Sequence
28	174.4	20.4	954	8	AF316419	AF316419 Lolium pe
29	171.6	20.0	950	8	AF159882	AF159882 Oryza sat
30	168.8	19.7	597	8	AB024715	AB024715 Arabidops
31	168.8	19.7	886	8	AY065211	AY065211 Arabidops
32	168.4	19.7	613	8	AX478043	AX478043 Sequence
33	166.8	19.5	559	8	AY096515	AY096515 Arabidops
34	166.4	19.4	980	6	AX478011	AX478011 Sequence
35	164	19.2	109936	8	ATF9F13	AL080253 Arabidops
36	164	19.2	197568	8	ATF145259	AF145259 Arabidops
37	160.6	18.8	577	8	AF145259	AF145259 Nicotiana
38	159.4	18.0	902	6	AX478009	AX478009 Sequence
39	159	18.4	907	8	AF159883	AF159883 Oryza sat
40	157.6	18.1	1295	6	AX478021	AX478021 Sequence
41	154.8	18.0	560	8	AF145260	AF145260 Nicotiana
42	154.4	18.0	869	8	LEU84140	LEU84140 Lycopersicon
43	146.8	17.1	558	8	AF145261	AF145261 Nicotiana
44	145.8	17.0	4377	8	ATU87834	ATU87834 Arabidopsis
45	136	15.9	354	8	AF145262	AF145262 Nicotiana

ALIGNMENTS

RESULT 1				
ARI48907				
LOCUS	ARI48907	856 bp	DNA	linear PAT 08-AUG-2001
DEFINITION	Sequence 3 from patent US 6225530.			
ACCESSION	ARI48907			
VERSION	ARI48907.1	GI:15112997		
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (Bases 1 to 856)			
TITLE	Weigel,D. and Kardal'sky,I. Flowering locus T (FT) and genetically modified plants having modulated flower development			
JOURNAL	Patent : US 6225530-A 3 01-MAY-2001;			

FEATURES Location/Qualifiers
source 1..856
/organism="unknown"
BASE COUNT 249 a 194 c 150 g 263 t
ORIGIN

Query Match 100.0%; Score 856; DB 6; Length 856;
Best Local Similarity 100.0%; Pred. No. 7.1e-192;
Matches 856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 CTCGAGTTTTTTTTTTTTTTTTTTTATTAATATAACATCTATTCAGTAGATTAA 60
DB 1 CTCGAGTTTTTTTTTTTTTTTTTTTATTAATATAACATCTATTCAGTAGATTAA 60
OY 61 TAATATGCGATCACACACTATATAAGTAAACACTCTCATTTCTCCCTCTCATTT 120
DB 61 TAATATGCGATCACACACTATATAAGTAAACACTCTCATTTCTCCCTCTCATTT 120
OY 121 TTATTACACACTTATATATGAACTATATAGCATCATACCCGTTCTGTTACTGTATCA 180
DB 121 TTATTACACACTTATATATGAACTATATAGCATCATACCCGTTCTGTTACTGTATCA 180
OY 181 TAAATGGTTATTAATTAATTAATATAGATGATGATGATGATGATGATGATGAT 240
DB 181 TAAATGGTTATTAATTAATTAATATAGATGATGATGATGATGATGATGATGAT 240
OY 241 CAATTGGTTATTAAGGAAGAACCATCTAAAGTCTCTCTCCGAGCCACTCTCCCTC 300
DB 241 CAATTGGTTATTAAGGAAGAACCATCTAAAGTCTCTCTCCGAGCCACTCTCCCTC 300
OY 301 TGACATTTGTATAAAACCTGCGCCACGCGGAGGAGGAGGAGGAGGAGGAGGAGG 360
DB 301 TGACATTTGTATAAAACCTGCGCCACGCGGAGGAGGAGGAGGAGGAGGAGGAGG 360
OY 361 CGAGTGTGAAGTTCTGGCGCCACCCTGGTGCATACACATGTTGCTGCGCAAGCTGTGA 420
DB 361 CGAGTGTGAAGTTCTGGCGCCACCCTGGTGCATACACATGTTGCTGCGCAAGCTGTGA 420
OY 421 AACCAATATTAACACGACAGATGAATTCCTGCAAGTGGACTTGGATTTTCGTAAACACA 480
DB 421 AACCAATATTAACACGACAGATGAATTCCTGCAAGTGGACTTGGATTTTCGTAAACACA 480
OY 481 ATCTATTTGCCAAAGGTTGTTCCAGTTGTAGCAGGAGATATCAGTACCAACCAATGAGAGA 540
DB 481 ATCTATTTGCCAAAGGTTGTTCCAGTTGTAGCAGGAGATATCAGTACCAACCAATGAGAGA 540
OY 541 TATTCCTGGAGGTGAGGGTGTCTAGAGACTTGGACATGCGATGCAACCAATGAGAGA 600
DB 541 TATTCCTGGAGGTGAGGGTGTCTAGAGACTTGGACATGCGATGCAACCAATGAGAGA 600
OY 601 TAGAAGTTCCTGAGGTCTCTCTCCACCAATCTCACTCTGCTGTTTGAACCTGAGAA 660
DB 601 TAGAAGTTCCTGAGGTCTCTCTCCACCAATCTCACTCTGCTGTTTGAACCTGAGAA 660
OY 661 GGCCTTAGATCCAAAGGTTTCTCAGCTCTCTTGGCCATAAGTAACCTTTAGAGATTT 720
DB 661 GGCCTTAGATCCAAAGGTTTCTCAGCTCTCTTGGCCATAAGTAACCTTTAGAGATTT 720
OY 721 GATCTATTAAAGGATCAAGAGATGCTCCACAACCTCTGCTTACATATAAGAGGCTCTTT 780
DB 721 GATCTATTAAAGGATCAAGAGATGCTCCACAACCTCTGCTTACATATAAGAGGCTCTTT 780
OY 781 ATATTATATAGACATTTTATGATCTTAAACAAACCTGCTGTAATTCCTGACCGGGGG 840
DB 781 ATATTATATAGACATTTTATGATCTTAAACAAACCTGCTGTAATTCCTGACCGGGGG 840
OY 841 ATCCACTAGTCTAGA 856
DB 841 ATCCACTAGTCTAGA 856
```

RESULT 2
AR148906/c

LOCUS AR148906 855 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6225530.
ACCESSION AR148906
VERSION AR148906.1 GI:15112996
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 855)
AUTHORS Weigel, D. and Kardalisky, I.
TITLE Flowering locus T (FT) and genetically modified plants having modulated flower development
JOURNAL Patent: US 6225530-A 1 01-MAY-2001;
FEATURES Location/Qualifiers
source 1..856
/organism="unknown"

BASE COUNT 263 a 151 c 193 g 248 t
ORIGIN
Query Match 98.4%; Score 842.4; DB 6; Length 855;
Best Local Similarity 99.8%; Pred. No. 1.2e-188;
Matches 854; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```
OY 1 CTCGAGTTTTTTTTTTTTTTTTTTTATTAATATAACATCTATTCAGTAGATTAA 60
DB 855 CTCGAGTTTTTTTTTTTTTTTTTTTATTAATATAACATCTATTCAGTAGATTAA 796
OY 61 TAATATGCGATCACACACTATATAAGTAAACACTCTCATTTCTCCCTCTCATTT 120
DB 795 TAATATGCGATCACACACTATATAAGTAAACACTCTCATTTCTCCCTCTCATTT 736
OY 121 TTATTACACACTTATATATGAACTATATAGCATCATACCCGTTCTGTTACTGTATCA 180
DB 735 TTATTACACACTTATATATGAACTATATAGCATCATACCCGTTCTGTTACTGTATCA 676
OY 181 TAAATGGTTATTAATTAATTAATATAGATGATGATGATGATGATGATGATGAT 240
DB 675 TAAATGGTTATTAATTAATTAATATAGATGATGATGATGATGATGATGATGAT 616
OY 241 CAATTGGTTATTAAGGAAGAACCATCTAAAGTCTCTCTCCGAGCCACTCTCCCTC 300
DB 615 C-ATTGGTTATTAAGGAAGAACCATCTAAAGTCTCTCTCCGAGCCACTCTCCCTC 557
OY 301 TGACATTTGTATAAAACCTGCGCCACGCGGAGGAGGAGGAGGAGGAGGAGGAGG 360
DB 556 TGACATTTGTATAAAACCTGCGCCACGCGGAGGAGGAGGAGGAGGAGGAGGAGG 497
OY 361 CGAGTGTGAAGTTCTGGCGCCACCCTGGTGCATACACATGTTGCTGCGCAAGCTGTGA 420
DB 496 CGAGTGTGAAGTTCTGGCGCCACCCTGGTGCATACACATGTTGCTGCGCAAGCTGTGA 437
OY 421 AACCAATATTAACACGACAGATGAATTCCTGCAAGTGGACTTGGATTTTCGTAAACACA 480
DB 436 AACCAATATTAACACGACAGATGAATTCCTGCAAGTGGACTTGGATTTTCGTAAACACA 377
OY 481 ATCTATTTGCCAAAGGTTTCTCAGTTGTAGCAGGAGATATCAGTACCAACCAATGAGAGA 540
DB 376 ATCTATTTGCCAAAGGTTTCTCAGTTGTAGCAGGAGATATCAGTACCAACCAATGAGAGA 317
OY 541 TATTCCTGGAGGTGAGGGTGTCTAGAGACTTGGACATGCGATGCAACCAATGAGAGA 600
DB 316 TATTCCTGGAGGTGAGGGTGTCTAGAGACTTGGACATGCGATGCAACCAATGAGAGA 257
OY 601 TAGAAGTTCCTGAGGTCTCTCTCCACCAATCTCACTCTGCTGTTTGAACCTGAGAA 660
DB 256 TAGAAGTTCCTGAGGTCTCTCTCCACCAATCTCACTCTGCTGTTTGAACCTGAGAA 197
OY 661 GGCCTTAGATCCAAAGGTTTCTCAGCTCTCTTGGCCATAAGTAACCTTTAGAGATTT 720
DB 196 GGCCTTAGATCCAAAGGTTTCTCAGCTCTCTTGGCCATAAGTAACCTTTAGAGATTT 137
OY 721 GATCTATTAAAGGATCAAGAGATGCTCCACAACCTCTGCTTACATATAAGAGGCTCTTT 780
DB 721 GATCTATTAAAGGATCAAGAGATGCTCCACAACCTCTGCTTACATATAAGAGGCTCTTT 780
```


TITLE
JOURNAL
REFERENCE
AUTHORS

Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shin, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.
Arabidopsis Full Length cDNA Clones
Unpublished
2 (bases 1 to 840)

TITLE
JOURNAL
COMMENT

Yamada, K., Ban, H., Chang, C.H., Chang, E., Dale, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shin, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.
Direct Submission
Submitted (04-DEC-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada, K., Ban, H., Chang, C.H., Chang, E., Dale, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shin, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.

Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.

FEATURES

source

1. 840
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/chromosome="1"
/clone="RAFL06-80-B19 (RI1796)"
/note="This clone is in a modified pBluescript vector (lambda ZAP) as a XhoI/SacI insert.
ecotype: Columbia"
1. 840
/gene="At1g65480"
1. 82
/gene="At1g65480"
83. 610
/gene="At1g65480"
/evidence="experimental"
/evidence="experimental"
/product="putative flowering signals mediating protein FT"
/protein_id="AA138919.1"
/db_xref="GI:17529186"
/translation="MSINRDLIVSRVGVLDLPNRSITLKVTYGGREYNGDLR
PSQVKNRPEVEIGEDLNFTLVVWDVDPSPDHLREYVHMLVTDLPATGTFG
NEIVCEYNSPTAGIHRVYFLFRLQGRQTVAPGMRQNFNREFAEIYNLPLPAAV
FYNCRESGCGGRRL"
611. 840
/gene="At1g65480"

3'UTR
BASE COUNT 276 a 148 c 182 g 234 t
ORIGIN

Query Match 89.2% Score 763.4 DB 8: Length 840;
Best Local Similarity 99.2% Pred. No. 5.4e-170;
Matches 767; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

40 TTCAATTCATGATGATTAATATATGCAATCAACACTATATAGTAAACACTGTC 99
|| ||| | | ||||||||||||||||||||||||||||||||||||||||||||

Db 837 TTTTITTTTTTTTGTATTAATATATGCAATCAACACTATATAGTAAACACTGTC 778
Qy 100 ATTTCTCCCTCCCTCTCAATTTTATTAACACTATATATGCAATCAACACTGTC 159
Db 777 ATTTCTCCCTCCCTCTCAATTTTATTAACACTATATATGCAATCAACACTGTC 718
Qy 160 CACCGTGTGTTACTGTTATCAATTAATGTTATTAATTAATTAATTAATTAATTAAT 219
Db 717 CACCGTGTGTTACTGTTATCAATTAATGTTATTAATTAATTAATTAATTAATTAAT 658
Qy 220 TCTCATGAGATGATCAATCAATTAATGTTATTAATGAGAAAGCAATCAATGTTCTT 279
Db 657 TCTCATGAGATGATCAATCAATTAATGTTATTAATGAGAAAGCAATCAATGTTCTT 598
Qy 280 CCTCCGACGACCTCTCCCTCTGACAAATTTGAGAAATCGGGCCGAGGAGGAGGAGG 339
Db 597 CCTCCGACGACCTCTCCCTCTGACAAATTTGAGAAATCGGGCCGAGGAGGAGGAGG 538
Qy 340 TTGTATGATCTGACCAATCTGCGAGTGTGAAGTTCTGCGCCACCTGTCATATCACT 399
Db 537 TTGTATGATCTGACCAATCTGCGAGTGTGAAGTTCTGCGCCACCTGTCATATCACT 478
Qy 400 GTTTGCTGCTGCAAGCTGTCGAAACATTAATTAACACGACATGATTTCTGCAAGTGG 459
Db 477 GTTTGCTGCTGCAAGCTGTCGAAACATTAATTAACACGACATGATTTCTGCAAGTGG 418
Qy 460 CTTCGATTTTCTGTAACACACATCTCATTTGCAAGGTTGTCAGTTGTGACGGGATA 519
Db 417 CTTCGATTTTCTGTAACACACATCTCATTTGCAAGGTTGTCAGTTGTGACGGGATA 358
Qy 520 TCACTACCAACCAATGAGATATTCGAGAGTGTGAGGTTGTCAGACTTGAACATCT 579
Db 357 TCACTACCAACCAATGAGATATTCGAGAGTGTGAGGTTGTCAGACTTGAACATCT 298
Qy 580 GGATCCACCAATTAACCAATGATTAATGATCTGAGGTTCTGTCACCAATCTCAATCTT 639
Db 297 GGATCCACCAATTAACCAATGATTAATGATCTGAGGTTCTGTCACCAATCTCAATCTT 238
Qy 640 GGCCTGTTTGAACCTGAGAGGCTTGAATCCAGGCTTATGACCTCTCTTGGCCA 699
Db 237 GGCCTGTTTGAACCTGAGAGGCTTGAATCCAGGCTTATGACCTCTCTTGGCCA 178
Qy 700 TAAGTAACCTTGAAGATGATGATCTATTAACGATCAAGACGTCCTCAACACTCTG 759
Db 177 TAAGTAACCTTGAAGATGATGATCTATTAACGATCAAGACGTCCTCAACACTCTG 118
Qy 760 CTTCATTAAGAGGCTCTTATATTAATTAATGACATCTTATCTTGAACAAAC 812
Db 117 CTTCATTAAGAGGCTCTTATATTAATTAATGACATCTTATCTTGAACAAAC 65
RESULT 5
AB027505/c 780 bp mRNA linear PLN 26-FEB-2000
LOCUS Arabidopsis thaliana FT (FLOWERING LOCUS T) mRNA, complete cds,
DEFINITION spliced variant.
ACCESSION AB027505
VERSION AB027505.1 GI:4903013
KEYWORDS FT.
SOURCE Arabidopsis thaliana (strain: Landsberg er) cDNA to mRNA.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1 (sites)
AUTHORS Kobayashi, Y., Kaya, H., Goto, K., Iwabuchi, M. and Araki, T.
TITLE A pair of related genes with antagonistic roles in mediating
JOURNAL flowering signals
MEDLINE Science 286 (5446), 1960-1962 (1999)
20050958
REFERENCE 2 (bases 1 to 780)
AUTHORS Araki, T. and Kobayashi, Y.
TITLE Direct Submission

to this work. Shinozaki, K. (RIKEN GSC) and rheologists, A. (SSP /PSEC) contributed equally to this work as PIs.
Location/Qualifiers
1. .559
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/chromosome="1"
/clone="U11796"
/note="This clone is in pUNI 51.
ecotype: Columbia"
1. .559
/gene="At1g65480"
1. .528
/gene="At1g65480"
/codon_start=1
/evidence=experimental
/product="putative flowering signals mediating protein FT"
/protein_id="AA091747.1"
/db_xref="GI:22136806"
/translation="MSINIRDPILVSVGVDPDLPNRSITLKYTGQREVNTGLDLR
PSQVQNPVREIGEDLRNFETLVVDVPSNPPLREYLRHMLYDIPATGTG
NEIYCENPSPITAGIHRVVFILFRQLGRQYARAGWQNFRTREAEIYNGLVAV
FYNGQRESCGGRL"
529. .559
/gene="At1g65480"
3' UTR
BASE COUNT 151 a 117 c 132 g 159 t
ORIGIN

Query Match 65.3%; Score 559; DB 8; Length 559;
Best Local Similarity 100.0%; Pred. No. 1.1e-121;
Matches 559; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 236 AATATCAATGCTTATAAGAGAGAGCATCTAAGCTTCTTCCCGCAGCCTCT 295
Db 559 AATATCAATGCTTATAAGAGAGAGCATCTAAGCTTCTTCCCGCAGCCTCT 500
QY 286 CCGCTGCAATTTGTAAAGAACTGGCGCCAGCGGAGCGGAGATTTAGATCTCAGCA 355
Db 499 CCGCTGCAATTTGTAAAGAACTGGCGCCAGCGGAGCGGAGATTTAGATCTCAGCA 440
QY 356 ACTGCGAGTGTGAAGTTGTGGCGCCACCGTGTGATACATCTTTGGCCGCAAGCT 415
Db 439 ACTGCGAGTGTGAAGTTGTGGCGCCACCGTGTGATACATCTTTGGCCGCAAGCT 380
QY 416 GTGCAACATATAAACAAGACAGATGAATTCCTGCAATGGAATTTGATTTGTAAC 475
Db 379 GTGCAACATATAAACAAGACAGATGAATTCCTGCAATGGAATTTGATTTGTAAC 320
QY 476 ACACAAATCTATGCAAGAGTTGTTCAGTTGTACAGAGATATCACTCACCAACAT 535
Db 319 ACACAAATCTATGCAAGAGTTGTTCAGTTGTACAGAGATATCACTCACCAACAT 260
QY 536 GAGATATTCGAGAGTGTGAGGTTGTAGAGCTTGAACAATCTGGATCCACCATTAACA 595
Db 259 GAGATATTCGAGAGTGTGAGGTTGTAGAGCTTGAACAATCTGGATCCACCATTAACA 200
QY 596 AAGTATAGAGTCTCTGAGTCTTCTCCACAATCTCACTTTGGCTTTGTTGAACCT 655
Db 199 AAGTATAGAGTCTCTGAGTCTTCTCCACAATCTCACTTTGGCTTTGTTGAACCT 140
QY 656 GAGAAGGCTTATGAGGCTTATGAGGCTTATGAGGCTTATGAGGCTTATGAGGCT 715
Db 139 GAGAAGGCTTATGAGGCTTATGAGGCTTATGAGGCTTATGAGGCTTATGAGGCT 80
QY 716 TGATTGATCTATTAAGAGGATCAAGAGCTCTCCAAACAATCTGTTACTATTAAGAGGT 775
Db 79 TGATTGATCTATTAAGAGGATCAAGAGCTCTCCAAACAATCTGTTACTATTAAGAGGT 20
QY 776 CTCTTATATTTATAGACAT 794
Db 19 CTCTTATATTTATAGACAT 1

RESULT 7
E38985/c 528 bp DNA linear PAT 31-JAN-2002
LOCUS
DEFINITION Method for shortening plant generation and plant.
ACCESSION E38985
VERSION E38985.1 GI:18625004
KEYWORDS JP 2000139250-A/1.
SOURCE
ORGANISM Arabidopsis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae.
REFERENCE
1 (bases 1 to 528)
Araki, T., Kobayashi, K., Ogawa, K. and Shirai, M.
Method for shortening plant generation and plant
patent: JP 2000139250-A 1 23-MAY-2000;
JOURNAL TORAY IND INC
OS Arabidopsis
PN JP 2000139250-A/1
PD 23-MAY-2000
PE 11-NOV-1998 JP 1998320219
PR

PI TAKASHI ARAKI, KYOJI KOBAYASHI, KENICHI OGAWA, MAKOTO SHIRAI PC
A01H1/00, A01H5/00, C12N5/10, C12N15/09, C12N5/10, C12R1:91, PC
(C12N15/09, C12R1:91), C12N5/00, C12N15/00, (C12N5/00, C12R1:91), PC
(C12N15/00, C12R1:91)
CC

FEATURES
source location/Qualifiers
FT source 1.528 /organism="Arabidopsis"
FT 1.528 /organism="Arabidopsis"

BASE COUNT 143 a 111 c 129 g 145 t
ORIGIN

Query Match 61.7%; Score 528; DB 6; Length 528;
Best Local Similarity 100.0%; Pred. No. 2.4e-114;
Matches 528; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 267 CTAAAGTCTTCTCTCCGCGACCCCTCTCCTGACAAATTTGTGAAGAACTCGCGCCAC 326
Db 528 CTAAAGTCTTCTCTCCGCGACCCCTCTCCTGACAAATTTGTGAAGAACTCGCGCCAC 469
QY 327 GGAAGGCCGAGATTTGTATGATCTCAGCAAACTCGGAGTGTGAAGTTCTGGCGCCACC 386
Db 468 GGAAGGCCGAGATTTGTATGATCTCAGCAAACTCGGAGTGTGAAGTTCTGGCGCCACC 409
QY 387 TGTGATACACTGTTTCTGCTCCCAAGCTGTGAAAACAATATAACAGACAGATGAAT 446
Db 408 TGTGATACACTGTTTCTGCTCCCAAGCTGTGAAAACAATATAACAGACAGATGAAT 349
QY 447 TCTTCGATGAGGACTTGTGATTTGTGACACACAATCTCATTTGCCAAAGTTTTCACGT 506
Db 348 TCTTCGATGAGGACTTGTGATTTGTGACACACAATCTCATTTGCCAAAGTTTTCACGT 289
QY 507 TGTACAGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 566
Db 288 TGTACAGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 229
QY 567 ACTTGAACATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 626
Db 228 ACTTGAACATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 169
QY 627 AATCTCACTCTTGGCTTTTGTGAAGCTGAGAAGGCTTATGATGATGATGATGATGAT 686
Db 168 AATCTCACTCTTGGCTTTTGTGAAGCTGAGAAGGCTTATGATGATGATGATGATGAT 109
QY 687 CTCTTTGGCGATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 746
Db 108 CTCTTTGGCGATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 49

09 747 TCCACACTGCTTACTATAGAGGCTCTTATATTATAGACAT 794
|||||
Db 48 TCCACACTGCTTACTATAGAGGCTCTTATATTATAGACAT 1
|||||

RESULT 8
F5114 109560 bp DNA linear PLN 11-JUN-1997
LOCUS F5114/C
DEFINITION Sequence of BAC F5114 from Arabidopsis thaliana chromosome 1,
complete sequence.
AC001229
AC001229.1 GI:2182285
KEYWORDS HTG.
SOURCE Arabidopsis thaliana.
ORGANISM Arabidopsis thaliana.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 109560)
Vysotskaya, V.S., Osborne, B.I., Toriumi, M., Yu, G., Oji, O.,
Shen, Y.K., Buehler, E., Conway, A.B., Conway, A.R., Dewar, K., Feng, J.,
Kim, C., Kurtz, D., Li, Y., Shinn, P., Sun, H., Davis, R.W., Ecker, J.R.,
Fedorov, N.A. and Theologis, A.
The sequence of BAC F5114 from Arabidopsis thaliana chromosome 1
Unpublished (1997)
2 (bases 1 to 109560)
Theologis, A.
Direct Submission
Submitted (17-APR-1997) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
3 (bases 1 to 109560)
Theologis, A.
Direct Submission
Submitted (17-APR-1997) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
4 (bases 1 to 109560)
Theologis, A.
Direct Submission
Submitted (06-JUN-1997) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
5 (bases 1 to 109560)
Theologis, A.
Direct Submission
Submitted (11-JUN-1997)
On Jun 10, 1997 this sequence version replaced gi:1943864.
COMMENTS Location/Qualifiers
1. 109560
/organism="Arabidopsis thaliana"
/cultivar="Columbia"
/db_xref="taxon:3702"
/chromosome="1"
/gene="F5114.1"
complement(join(129..327,950..1191))
/gene="F5114.1"
/codon_start=1
/evidence=not_experimental
/protein_id="AAB60919.1"
/db_xref="GI:2190555"
/translation="MRQPKSELPKLTISGVTSDGEPNMEKGDGCEENNEDGR
OCKPSSNRKSRVAKKOLDFKSCPGFGYGIIMPSTGFLNITKDHAWIKILLYKK
LYKAFQIVKMKTKYWKVKVORLMMKIMYKMLCMDSQKMR"
complement(1312..2949)
/gene="F5114.2"
complement(join(1312..1701,1833..1956,2039..2186,
2268..2367,2491..2949))
/gene="F5114.2"
/codon_start=1
/evidence=not_experimental
/protein_id="AAB60903.1"
/db_xref="GI:2190539"
/translation="MDEVSTVENENRKMIMIEPKLKKRRREPTAIENTLSEKESQI
SLNLEMKGLFDYFREVMDKSKRTDLFSGFSCSSINSVALLMEEMSLPLSKLVDEI

gene
CDS
10580..12759
/gene="F5114.3"
join(10580..10780,11596..11657,12371..12411,12536..12759)
/gene="F5114.3"
/note="Similar to Arabidopsis TFL1 (gb|U77674)."
/codon_start=1
/evidence=not_experimental
/protein_id="AAB60904.1"
/db_xref="GI:2190540"
/translation="MSINTRDPLYSRVYGVLDLPNRSITLKYTGQREYNGDLR
PVOVKRPFVEGGEDLNRFYLVVDPVPSPNHLLEYLHMLTDLIPATGTFG
NIVCYENSPSPGAIHRYVYILFRLGRQTVYAPGWRQNTREFAEIYNGLPVAAY
FYNCQRESCGGRRL"
36957..37445
/gene="F5114.4"
join(36957..37065,37294..37445)
/gene="F5114.4"
/codon_start=1
/evidence=not_experimental
/protein_id="AAB60905.1"
/db_xref="GI:2190541"
/translation="MGKSPNTAAEMLPLLLILFTLSQDKYVESGRKLAMGFSGTP
IYVTPSRSGTSPAVFTSKMRPRCPSPSYIPASQSP"
complement(40241..40963)
/gene="F5114.5"
complement(40241..40963)
/gene="F5114.5"
/codon_start=1
/evidence=not_experimental
/protein_id="AAB60906.1"
/db_xref="GI:2190542"
/translation="MCSLEKRDRLFLIKLTGGEHRLNPLTDSLRSTINOIRSDPSF
SOSVLTITSDGKFFSGDYDLAELSPSISYWDATRLSVADLISLPMTAAVYGH
ASAGCITLASHDYLMRDRGFLYSELDLILVPMWYATRGITGSPAAARDVWL
TAAKYADYGVKMGIVDSAYGSAETVEAIIKIGEBIYVRGGDGHYGMKRSLLREV
LIHTIGYESGSSVYRSTGSKL"
complement(41498..42875)
/gene="F5114.6"
complement(join(41498..41562,41619..41734,41808..41896,
41981..42127,42220..42267,42316..42564,42795..42875))
/gene="F5114.6"
/note="EST gb|N37484 comes from this gene."
/codon_start=1
/evidence=not_experimental
/protein_id="AAB60907.1"
/db_xref="GI:2190543"
/translation="MAGKLKPEEAVQATLSLPEDEVVDYGEDEEEDDEEMAKMKEESA
SOKDVALDEMASTAKDANEOAKKATLEKHEBCLISRALVLAASVYRLITLTISF
ILPILGIVRSVMSREPEFLTKVEKVDYMSGGTGDDEEDRKAYLAERDSDSA
OKRIADKTSNALIDRVYIMLQKLEKIIDVDYDKTDEEDLRSDSVYDYDKVSDDEVAL
AAATLKDTLGEKTIQELIOLVLSKDKVFYVFRMONTGRLSEVSRP"
complement(42975..44922)
/gene="F5114.7"
complement(join(42975..43043,43213..43339,43501..43593,
43683..43771,43856..44002,44168..44480,44564..44922))
/gene="F5114.7"
/note="Similar to Saccharomyces hypothetical protein
p9642.2 (gb|U40828)."
/codon_start=1
/evidence=not_experimental
/protein_id="AAB60908.1"
/db_xref="GI:2190544"
/translation="MEGYRSLQSPSNGYGLIELPYPLCYRVPSWYSLSATA
NKPBDHKGKGVTSQTRKASPEECDAVSGLSLAKAKAKAMKEESQSDISIMQVR
LPLGIGPALRAIASRDMWAKRLKMDDEFSTLQHWLKGKRLMAVRYLSIVRLV
KLANGGLSRREOQLTRTADIFRLVPAVAVIIVPMFLLVPFLKLPNNMIPSTFO
DKMKREELARRLNAIMEYAKFLQDTVKEMAKVQVRSRGEIKKTAEDLDGFWTKVR

gene	complement(47061. .49870)	complement(join(47061. .47422,47541. .47632,47766. .47824,47929. .48015,48122. .48218,48320. .48525,48704. .48799. .48884. .48959,49053. .49153,49242. .49418,49467. .49532,49587. .49654,49750. .49870))
CDS	/gene="F5114.8"	/note="Similar to Zea mays permealase 1 (gb U43034)."
gene	/codon_start=1	/evidence=not_experimental
CDS	/protein_id="AAB60909.1"	/db_xref="GI:2190545"
gene	/translation="MTNGGGGNNNAARTELQHPYKEQDLPGLQICVNSPPWLEAVVLGPHYLLLSGITVLIPSMLETFEFFFFEFLNLSLITAYARXVATQTLLEVSGLTFLFQSEFETRLPVAIVASVAYIIPITISITSTRVTYDPERFRVMSIQCALITGCFQVLLILCWNRNIVAFSLPSLIAPLAFETGTHIDEPFLIYNNMOTSFYQIARCEVVALPCLILFVTOGLPREFLKKRGGVNLIDSCDRGMILCIPVLWAFQOLTS SGVVDKHSHTTQGTGCRDRGLINTFPWIIIPYFQMGSPPTQITQSPAMASPYTLFPTSGIPASARVGSATPIPPSVYSRKTCHMGVGLNGLMGITGTTTSTENVGLAMTKISRRVIOISAFEMIFSIKGFCAFPASIPLPIMASLYCIVLCEVKSSSHII CSIAISINQIISFETFKIKSNSTIVAAVGLSYLOFCMLNSFNIRKILGSEFMAISIP OYFREYVNGWRSDHSHSNWTSYSIL"	/complement(50678. .52743)
CDS	/gene="F5114.9"	complement(join(50678. .51059,51406. .51488,51567. .51733,51818. .52033,52078. .52294,52510. .52743))
gene	/gene="F5114.9"	/note="Strong similarity to Arabidopsis zeta-crystallin-like protein (gb I49268)."
CDS	/codon_start=1	/evidence=not_experimental
gene	/protein_id="AAB60917.1"	/db_xref="GI:2190553"
CDS	/translation="MGEYSVYENKRVILKNYVDGIPTETDMEVKLGTEILKAPKSSCFIVNLTILSCDPMYRGMGRDHFSGSYLPYPVQGCCVEVRLFELGELFEEREGRCIYALERTSPFRCGEDMIYMLRKLCELYLAKLLEIFPNDLSLIDSPVITLMO RIEGGIARVDSDDPNYKRGDIIVSGILIGMEYSILRSSNLDLRNIQDDPIPSYH LGILGMAGFTIYAGFNEICCPKRGDSYFVSNACGAVQGLQAKLHGCTGVGSASK GKVELLKQELIDAEFNKREADDITVALRYKPEPGIDIPYDNGGSMALDANMKVR GRVALCGVSLQSLSTSSQIKNLYSAYIKRLRLEGLDQIVLHIFPOPLENKKRYK EGGIYVYEDISEGDLAPALVGLGFSKKNIGKQVRAKE"	complement(53168. .54916)
gene	/gene="F5114.10"	complement(join(53168. .53386,53396. .54114,54461. .54916))
CDS	/gene="F5114.10"	/note="Strong similarity to solanum polygalacturonase precursor (gb U23053)."
gene	/codon_start=1	/product="F5114.10"
CDS	/protein_id="AAB60920.1"	/db_xref="GI:2190556"
gene	/translation="MALFISFVQVFSIVITIIMSHFGQFARTSLNVLSEGANPNIV ESAAFLSAPMAACGVDSVYIVYKGRVYSGVREGSGKSNCGNCPGEGATLIPD LQYASATLCKEMWFSGVHNVTYVKGSGFQKSGTMSKAGNCPGEGATLIPDNDN NVTIKGVYSLNSQLPHAIINRCRIKRIEDVRIIAPDESPDTGDIHILQSLDIENNAS IKTGDDCSISDEGTKNLMDGICITGPHGHSIGSLASILEQGVENVYVKNAAVFVTD NGLRISIPRHSNGEVRVRFGLAIVGNVSPYLIDQNCQPDGSCPSQESGKINDV IYSIMGTSATREIAIKKMCEKVPCTGIRMQAINTISYCGAATCTSNVSGQLGLVY	
Match	54.4%	Score 466; DB 8; Length 109560;
Local Similarity	100.0%	Ident. No. 8.3e-100; Indels 0; Gaps 0;
Conservative	0;	Mismatches 0;

QY	26	TATTAATATTAACACCTCATTTTCATGAGATATATATTAATATTCGGATCACACATTTATA	85
Db	13000	TATAATATTAACACCTCATTTTCATGAGATATATATTAATATTCGGATCACACATTTATA	12944
QY	86	AGTAAACACCTCTCATTTCCGCCGCCCTCTCATTTTATTACACACTTATATATGAGCT	145
Db	12940	AGTAAACACCTCTCATTTCCGCCGCCCTCTCATTTTATTACACACTTATATATGAGCT	12881

QY	146	ACTATAGGATATCATCCGTTGTTACCTGCTACGCTATCAATTAATGTTAAATTAATAC	205
Db	12880	ACTATAGGATATCATCCGTTGTTACCTGCTACGCTATCAATTAATGTTAAATTAATAC	12821
QY	206	TATAGATGATTAATCTCATCAGAGTATGCAATTAATCAATGGTTATTAAGAAGAACCA	265
Db	12820	TATAGATGATTAATCTCATCAGAGTATGCAATTAATCAATGGTTATTAAGAAGAACCA	12761
QY	266	TCTAAGTCTTCTCTCCGCGACACTCTCCCTGACAAATTTGTAAGAAATCGGGGCA	325
Db	12760	TCTAAGTCTTCTCTCCGCGACACTCTCCCTGACAAATTTGTAAGAAATCGGGGCA	12701
QY	326	CGGGAAGCCGAGATTTAGATCTCAGCAAACTCGCGAGTGTGGAAGTTCTGGCCACC	385
Db	12700	CGGGAAGCCGAGATTTAGATCTCAGCAAACTCGCGAGTGTGGAAGTTCTGGCCACC	12641
QY	386	CTGGTCATATCACTGTTTGCTGCGCAAGCTGTGCAAAATTAACACGACAGATGA	445
Db	12640	CTGGTCATATCACTGTTTGCTGCGCAAGCTGTGCAAAATTAACACGACAGATGA	12581
QY	446	TTCCGTCAGTGGAGCTTGATTTTGTTGTAACACAAATCTCATTTGCC	491
Db	12580	TTCCGTCAGTGGAGCTTGATTTTGTTGTAACACAAATCTCATTTGCC	12535
RESULT	9		
LOCUS	AF152096/c	2483 bp	DNA linear
DEFINITION	Arabidopsis thaliana flowering locus T (FT) gene, complete cds.		PLN 22-DEC-1999
ACCESSION	AF152096		
VERSION	AF152096.1	GI:6117977	
KEYWORDS			
SOURCE	Arabidopsis thaliana.		
ORGANISM	Arabidopsis thaliana.		
REFERENCE	Eukariota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 2483) Kardalisky, I., Shukla, V.K., Ahn, J.H., Dagenais, N., Christensen, S.K., Nguyen, J.T., Chory, J., Harrison, M.J. and Weigel, D.		
AUTHORS	Activation tagging of the floral inducer FT Science 286 (5446), 1962-1965 (1999)		
TITLE	2 (bases 1 to 2483)		
JOURNAL	Kardalisky, I. and Weigel, D.		
PUBMED	Direct Submission		
REFERENCE	Submitted (17-MAY-1999) Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA		
AUTHORS	Location/Qualifiers		
TITLE	1. 2483		
JOURNAL	/organism="Arabidopsis thaliana"		
PUBMED	/cultivar="Columbia"		
REFERENCE	/db_xref="taxon:3702"		
AUTHORS	/chromosome="I"		
TITLE	/map="90 CM; F5114"		
JOURNAL	1. 2483		
PUBMED	/gene="FT"		
REFERENCE	join(1. 264,1080. 1141,1855. 1895,2020. 2483)		
AUTHORS	/gene="FT"		
TITLE	/product="flowering locus T"		
JOURNAL	1. 63		
PUBMED	/gene="FT"		
REFERENCE	join(64. 264,1080. 1141,1855. 1895,2020. 2243)		
AUTHORS	/gene="FT"		
TITLE	/function="induces flowering"		
JOURNAL	/note="similar to hippocampal cholinergic neurostimulating peptide (HCNP) precursor, phosphatidylethanolamine binding protein (PEBP) and Raf kinase inhibitor protein;		
PUBMED	corresponds to Arabidopsis thaliana BAC F5114 sequence		
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			

presented in GenBank Accession Number AC001229)
/codon_start=1
/product="flowering locus T"
/protein_id="AA03936.1"
/db_xref="GI:6117978"
/translation="MSINRDLIVSRVGVGLDFPNRSITFLKVTYGGORETNGCLDL
PSOVONKPEVLGEGDLRNEFTLVAVDDVDSPSNPHLREVLIVYDIPATGTFGG
NIVCYENSPAGIGHRVVFLFRQLGQIYVAPQWRNENFTREAFELIYNGLVAAVA
FYNCORESCGGGRLL"
2483

OY 690 TCTTTGGCCATAGTACCTTTAGAGTATGATCTATTTAAACGATCAAGACGCTGCC 749
 Db 136 TCTATGGCCATTAAGTACGATTAAGAGACCAACCTCGTGAAGATCAAGAACATCTCC 77
 OY 750 AACAACTGCTGCTACTATAGAGGCTCTCTATATTATTAAGACATCTTGACTTGAAAC 808
 Db 76 AACAACTGCGACGACCAAGAGATCTCTACGACTTAAGACATATTATCTTGATTC 18
 RESULT 11
 AF152907/c 528 bp mRNA linear PLN 22-DEC-1999
 LOCUS Arabidopsis thaliana twin sister of FT (TSF) mRNA, complete cds.
 DEFINITION AF152907
 VERSION AF152907.1 GI:6117979
 KEYWORDS
 SOURCE Arabidopsis thaliana.
 ORGANISM Arabidopsis thaliana.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 528)
 Kardalisky, I., Shukla, V.K., Ahn, J.H., Dagenais, N.,
 Christensen, S.K., Nguyen, J.T., Chory, J., Harrison, M.J. and
 Weigel, D.
 Activation tagging of the floral inducer FT
 Science 286 (5446), 1962-1965 (1999)
 JOURNAL MEDLINE 20050959
 PUBMED 10583961
 REFERENCE 2 (bases 1 to 528)
 Haakma, S., Shukla, V.K., Ahn, J.H. and Weigel, D.
 Direct Submission
 Submitted (19-MAY-1999) Plant Biology Laboratory, The Salk
 Institute for Biological Studies, 10010 N. Torrey Pines Road, La
 Jolla, CA 92037, USA
 FEATURES
 source location/Qualifiers
 1..528
 /organism="Arabidopsis thaliana"
 /cultivar="Columbia"
 /db_xref="taxon:3702"
 /chromosome="IV"
 /map="between g3883 and g13836"
 1..528
 /gene="TSF"
 /gene="TSF"
 1..528
 /gene="TSF"
 /note="flowering locus T (FT) homolog: similar to
 hippocampal cholinergic neurostimulating peptide (HCNP)
 precursor, phosphatidylethanolamine binding protein (PEBP)
 and Raf kinase inhibitor protein"
 /codon_start=1
 /product="twin sister of FT"
 /protein_id="AA03937.1"
 /db_xref="GI:6117980"
 /translation="MSLSRDPLVGSVDVDLPTRLVSLKTYGSHREYNGLDLR
 PSQVLPKPIVEIGDDDEIRNFYTLVMDPDPVSPSPHORELHMLVTIDPATGNAG
 NEVVCESPPSPGIRHIVLVEFROLGRQTVAYAGMRQNTREFAEIYNGLPVAAS
 YFNCORENGCGGRRRT"
 BASE COUNT 123 a 116 c 142 g 147 t
 ORIGIN
 Query Match 44.1%; Score 377.6; DB 8; Length 528;
 Best Local Similarity 82.2%; Pred. No. 8.3e-79;
 Matches 434; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

OY 387 TGGTCATACACTGTTTGCCTGCCAAGCTGTGGAACATATATAACGACGATGAT 446
 Db 408 CGGTGCAATAAACCGTTTGTCTCCAGTTGCCGGAACAATACCAACAAATGATGAT 349
 OY 447 TCCCTGAGTGGGACTTGGATTTTCTGAACACCAATCTCATTTGCCAAGGTTGTTCCAGT 506
 Db 348 TCCCGAGGGGGGACGTGTCTGTACACACCAACCTCATTTGCCAAGGCAATTTCCAGT 289
 OY 507 TGTACGAGGATATGATGATCACCACCAATGAGATATTTCTGAGGTAGGTTGCTAGG 566
 Db 288 GGTGCGAGGTATATGATGATGATCACCACCAAGTGGAGATATTTCTGTTAGGTTGCTAGG 229
 OY 567 ACTTGAACATCTGATGATCACCACCAATGAGATATGAGGTTGCTGAGGTTCTTCCACC 626
 Db 228 ACTCGGACATCTGATGATCACCACCAATGAGATATTTCTGAGGTTGCTGAGGTTCTTCC 169
 OY 627 ATCTCACTCTGCTGCTTTGTAACCTGAGAGGCTTGTATGATCCAGGCTTGTGAC 686
 Db 168 ATCTCACTATGTTGTTGTTGTAACCTGAGAGGCTTGTATGATCCAGGCTTGTGAC 109
 OY 687 CTCTCTTGGCCATAGTAACTTTAGAGTATGATGATTTAAAGGATCAAGACGTC 746
 Db 108 CTCTCTATGCGCATATAGTAACTTTAGAGTATGATGATTTAAAGGATCAAGACATC 49
 OY 747 TCCAACAACCTGCTTACTATAGAGGCTCTCTATATTTATATAGACAT 794
 Db 48 TCCAACAACACTGCGGACCAAGAGATCTCTACGACTTAAGACAT 1
 RESULT 12
 E38986/c 528 bp DNA linear PAT 31-JAN-2002
 LOCUS E38986
 DEFINITION Method for shortening plant generation and plant.
 ACCESSION E38986
 VERSION E38986.1 GI:18625005
 KEYWORDS JP 2000139250-A/2.
 SOURCE Arabidopsis.
 ORGANISM Arabidopsis.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae.
 1 (bases 1 to 528)
 Araki, T., Kobayashi, K., Ogawa, K. and Shirai, M.
 Method for shortening plant generation and plant
 Patent: JP 2000139250-A 2 23-MAY-2000;
 TORAY IND INC
 JOURNAL
 REFERENCE OS Arabidopsis
 AUTHORS PN JP 2000139250-A/2
 TITLE PD 23-MAY-2000
 JOURNAL PF 11-NOV-1998 JP 1998320219
 COMMENT PR
 PI TAKASHI ARAKI, KYOJI KOBAYASHI, KENICHI OGAWA, MAKOTO SHIRAI PC
 A01H1/00, A01H5/00, C12N5/10, C12N5/09, C12N5/10, C12R1/91, PC
 (C12N5/09, C12R1/91), C12N5/00, C12N5/00, (C12N5/00, C12R1/91), PC
 (C12N5/00, C12R1/91)
 CC
 FH key Location/Qualifiers
 FT source 1..528
 FT location/Qualifiers
 1..528
 /organism="Arabidopsis"
 /db_xref="taxon:3701"
 BASE COUNT 122 a 117 c 142 g 147 t
 ORIGIN
 Query Match 43.7%; Score 374.4; DB 6; Length 528;
 Best Local Similarity 81.8%; Pred. No. 4.7e-78;
 Matches 432; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

XX WPI: 1999-611305/52.
 DR P-PSDB; AA49098.
 XX
 XX
 PT New flowering locus T polypeptide that regulates flowering time,
 particularly used to accelerate flowering -
 XX
 XX
 PS Claim 5; Fig 2; 64pp; English.
 CC This sequence is the flowering locus T (FT) gene of Arabidopsis thaliana.
 CC FT regulates flowering in plants by modulating flowering time.
 CC Overexpression of FT results in early flowering, while loss of function
 CC mutations or antisense directed to FT causes late flowering. The FT
 CC polypeptide has a molecular weight of approximately 20kD, and is located
 CC on chromosome 1. The FT polypeptide is used in the invention to modulate
 CC flowering time in many mono and di-cotyledonous plants. The FT
 CC polynucleotide sequence is used for recombinant production of the
 CC polypeptide, and as a source of antisense, ribozyme or triplex forming
 CC sequences. The FT polypeptide can also be used to raise antibodies and to
 CC screen for modulators or cellular binding proteins. The methods of the
 CC invention allow for the production of crops at any time of year.
 CC
 SO Sequence 856 BP; 263 A; 150 C; 194 G; 249 T; 0 other;

Query Match 100.0%; Score 856; DB 20; Length 856;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 Matches 856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCGAGTTTATTAATAATACTTCAATTCATGATTAATA 60
 DB 856 CTCGAGTTTATTAATAATACTTCAATTCATGATTAATA 797
 QY 61 TAAATATCGATACACACATATATAAAGTAAACACTCTATTTCTCCCTCATTT 120
 DB 796 TAAATATCGATACACACATATATAAAGTAAACACTCTATTTCTCCCTCATTT 737
 QY 121 TTAATACACACTTATATATAGTAACTATAGGATCATACCGTTCGTTACTGTATCA 180
 DB 736 TTAATACACACTTATATATAGTAACTATAGGATCATACCGTTCGTTACTGTATCA 677
 QY 181 TAAATGTTTAAATTAATATATATAGTAACTATAGGATCATACCGTTCGTTACTGTATCA 240
 DB 676 TAAATGTTTAAATTAATATATATAGTAACTATAGGATCATACCGTTCGTTACTGTATCA 617
 QY 241 CAATGTTTAAAGGAGAGAGCCATTAAGTCTTCTCCGCGAGCCACTCTCCCTC 300
 DB 616 CAATGTTTAAAGGAGAGAGCCATTAAGTCTTCTCCGCGAGCCACTCTCCCTC 557
 QY 301 TGACATTTAGAAAACTCGGCGACGAGGAGCGGAGATTGTAGTCTCAGCAAACTCG 360
 DB 556 TGACATTTAGAAAACTCGGCGACGAGGAGCGGAGATTGTAGTCTCAGCAAACTCG 497
 QY 361 CGAGTGTAAAGTTCGGCGCCACCTGGTGATACACTGTTGGCTGGCAAGCTGTGA 420
 DB 496 CGAGTGTAAAGTTCGGCGCCACCTGGTGATACACTGTTGGCTGGCAAGCTGTGA 437
 QY 421 AACATATTAACACGACAGATGAATTCCTGCAAGTGGAGCTTGATTTTCGTAACACACA 480
 DB 436 AACATATTAACACGACAGATGAATTCCTGCAAGTGGAGCTTGATTTTCGTAACACACA 377
 QY 481 ATCTCATTTCCAAAGGTTTTCAGTGTAGCAAGGATATCAGTCTCACCACCAANTGAGA 540
 DB 376 ATCTCATTTCCAAAGGTTTTCAGTGTAGCAAGGATATCAGTCTCACCACCAANTGAGA 317
 QY 541 TATTCGCGAGGTGAGGGTGTAGGACTTGGACATCGATGCCAATTAACCAAGTA 600
 DB 316 TATTCGCGAGGTGAGGGTGTAGGACTTGGACATCGATGCCAATTAACCAAGTA 257
 QY 601 TAGAAGTTCCTGAGTCTCTCCACCAATCTCAACTCTGGCTGTTGTTGAACCTGAGAA 660
 DB 256 TAGAAGTTCCTGAGTCTCTCCACCAATCTCAACTCTGGCTGTTGTTGAACCTGAGAA 197
 QY 661 GGCCTTAGTCCAGGCAATTAAGTACCTCTCTTTGGCCATTAAGTAACCTTTAGAGTGAAT 720

DB 196 GGCCTTAGTCCAGGCAATTAAGTACCTCTCTTTGGCCATTAAGTAACCTTTAGAGTGAAT 137
 QY 721 GATCTATTAAGGATCAAGAACGCTCCACCAACGCTGCTACTATTAAGAGGCTCTT 780
 DB 136 GATCTATTAAGGATCAAGAACGCTCCACCAACGCTGCTACTATTAAGAGGCTCTT 77
 QY 781 ATATTTATAGACATCTTGTATCTTGAACAACCTCGCTGGAATTCCTCAGCCGGGG 840
 DB 76 ATATTTATAGACATCTTGTATCTTGAACAACCTCGCTGGAATTCCTCAGCCGGGG 17
 QY 841 ATCCACTAGTCTAGA 856
 DB 16 ATCCACTAGTCTAGA 1

RESULT 2
 AA28491
 ID AA28491 standard; cDNA; 856 BP.
 XX
 AC AA28491;
 XX
 DT 17-JAN-2000 (first entry)

XX Flowering locus T (FT) gene antisense insert.
 DE Flowering locus T gene; FT; flowering time; modulator; early flowering;
 XX antibody; cellular binding protein; crop; antisense construct; ss.
 KW Arabidopsis thaliana.

OS Arabidopsis thaliana.
 PN WO9953070-A1.

PD 21-OCT-1999.

PF 13-APR-1999; 99WO-US08151.

PR 15-APR-1998; 98US-0060726.

XX (SALK) SALK INST BIOLOGICAL STUDIES.

XX Weigel D;

DR WPI: 1999-611305/52.

PT New flowering locus T polypeptide that regulates flowering time,
 particularly used to accelerate flowering -

PS Example 2; Fig 3; 64pp; English.

XX This is the flowering locus T (FT) gene antisense polynucleotide
 CC sequence. This sequence is used in the production of the antisense
 CC construct of the invention PSK1060. FT regulates flowering in plants by
 CC modulating flowering time. Overexpression of FT results in early
 CC flowering, while loss of function mutations or antisense directed to FT
 CC causes late flowering. The FT polypeptide has a molecular weight of
 CC approximately 20kD, and is located on chromosome 1. The FT polypeptide is
 CC used in the invention to modulate flowering time in many mono and
 CC di-cotyledonous plants. The FT polynucleotide sequence is used for
 CC recombinant production of the polypeptide, and as a source of antisense,
 CC ribozyme or triplex forming sequences. The FT polypeptide can also be
 CC used to raise antibodies and to screen for modulators or cellular binding
 CC proteins. The methods of the invention allow for the production of crops
 CC at any time of year.

SO Sequence 856 BP; 249 A; 150 C; 194 G; 263 T; 0 other;

Query Match 100.0%; Score 856; DB 20; Length 856;
 Best Local Similarity 100.0%; Pred. No. 3.8e-190;
 Matches 856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCGAGTTTATTAATAATACTTCAATTCATGATTAATA 60
 |||

OS	Arabidopsis thaliana.
PN	FE1033405-A2.
XX	06-SEP-2000.
XX	25-FEB-2000; 2000EP-0301439
XX	25-FEB-1999; 9905-0123185
PR	05-MAR-1999; 9905-0123180
PR	09-MAR-1999; 9905-0123548
PR	23-MAR-1999; 9905-0125788
PR	23-MAR-1999; 9905-0126564
PR	23-MAR-1999; 9905-0126785
PR	01-APR-1999; 9905-0127462
PR	06-APR-1999; 9905-0128334
PR	08-APR-1999; 9905-0128714
PR	16-APR-1999; 9905-0129845
PR	13-APR-1999; 9905-0130047
PR	21-APR-1999; 9905-0130510
PR	23-APR-1999; 9905-0130891
PR	28-APR-1999; 9905-0131449
PR	30-APR-1999; 9905-0132048
PR	30-APR-1999; 9905-0132407
PR	04-MAY-1999; 9905-0132484
PR	05-MAY-1999; 9905-0132485
PR	06-MAY-1999; 9905-0132486
PR	07-MAY-1999; 9905-0132487
PR	07-MAY-1999; 9905-0132863
PR	11-MAY-1999; 9905-0134256
PR	14-MAY-1999; 9905-0134218
PR	14-MAY-1999; 9905-0134219
PR	14-MAY-1999; 9905-0134221
PR	14-MAY-1999; 9905-0134370
PR	18-MAY-1999; 9905-0134761
PR	19-MAY-1999; 9905-0134941
PR	20-MAY-1999; 9905-0135124
PR	21-MAY-1999; 9905-0135153
PR	24-MAY-1999; 9905-0135629
PR	25-MAY-1999; 9905-0136021
PR	27-MAY-1999; 9905-0136392
PR	28-MAY-1999; 9905-0136782
PR	01-JUN-1999; 9905-0137222
PR	03-JUN-1999; 9905-0137528
PR	04-JUN-1999; 9905-0137502
PR	07-JUN-1999; 9905-0137724
PR	08-JUN-1999; 9905-0138094
PR	10-JUN-1999; 9905-0138540
PR	10-JUN-1999; 9905-0138847
PR	14-JUN-1999; 9905-0139119
PR	16-JUN-1999; 9905-0139452
PR	16-JUN-1999; 9905-0139493
PR	17-JUN-1999; 9905-0139492
PR	18-JUN-1999; 9905-0139454
PR	18-JUN-1999; 9905-0139455
PR	18-JUN-1999; 9905-0139456
PR	18-JUN-1999; 9905-0139457
PR	18-JUN-1999; 9905-0139458
PR	18-JUN-1999; 9905-0139459
PR	21-JUN-1999; 9905-0139617
PR	22-JUN-1999; 9905-0139819
PR	23-JUN-1999; 9905-0140353
PR	23-JUN-1999; 9905-0140354
PR	24-JUN-1999; 9905-0140695
PR	28-JUN-1999; 9905-0140823
PR	29-JUN-1999; 9905-0140991

PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142820.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 28-JUL-1999; 99US-0145919.
PR 02-AUG-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0148368.
PR 17-AUG-1999; 99US-0148175.
PR 18-AUG-1999; 99US-0148426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.

PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159295.
PR 13-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 26-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 80.9%; Score 692.4; DB 21; Length 775;
Best Local Similarity 99.9%; Pred. No. 5.3e-152;
Matches 693; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 119 TTTTATTACACTTATATATATGACTACTATAGCATCATCACCCTTGTACTCTGAT 178
DB 758 TTTTATTACACTTATATATATGACTACTATAGCATCATCACCCTTGTACTCTGAT 699
QY 179 CATTAATGCTTATTAATTAATTAATCTATAGTCATTAATCTCATGAGTATGCAAT 238
DB 698 CATTAATGCTTATTAATTAATTAATCTATAGTCATTAATCTCATGAGTATGCAAT 639
QY 239 ATCAATGGTTATTAAGGAAGAGCCATCTAAAGTCTTCTCCGCGAGCCATCTCC 298
DB 638 ATCAATGGTTATTAAGGAAGAGCCATCTAAAGTCTTCTCCGCGAGCCATCTCC 579
QY 299 TCTGCAATTTGAAAGAAATGCGGCCGCGGAGGCGGAGATTTGATCTCAGCAAACT 358
DB 578 TCTGCAATTTGAAAGAAATGCGGCCGCGGAGGCGGAGATTTGATCTCAGCAAACT 519
QY 359 CCGAGTGTGAAGTCTGCGCGCACCCGTCGTCATACCTGTTTCCCGCAGCTGTC 418
DB 518 CCGAGTGTGAAGTCTGCGCGCACCCGTCGTCATACCTGTTTCCCGCAGCTGTC 459
QY 419 GAACATATTAACACGACGACGATGATCTCTGACAGTGGACTTGGATTTGTAACACA 478
DB 458 GAACATATTAACACGACGACGATGATCTCTGACAGTGGACTTGGATTTGTAACACA 399
QY 479 CAATCTCATTCGCAAGGTTGTCAGTTGACAGGATATCACTACCAACCAATGGA 538
DB 479 CAATCTCATTCGCAAGGTTGTCAGTTGACAGGATATCACTACCAACCAATGGA 538

Db 398 CAATCTATTGCCAAGGTTGCTCAGTTGACGAGGATATCATGCAACCAACATGCA 339
Qy 539 GATATTCGAGAGGTGAGGTTGCTAGACTTGAAATCGATGATCCACATTAACCAAG 598
Db 338 GATATTCGAGAGGTGAGGTTGCTAGACTTGAAATCGATGATCCACATTAACCAAG 279
Qy 599 TATAGAGTTCCGAGGTTCTCTCCACCAATCTCACTCTGCTTTGTTGAACCTGAG 658
Db 278 TATAGAGTTCCGAGGTTCTCTCCACCAATCTCACTCTGCTTTGTTGAACCTGAG 219
Qy 659 AAGGCTTAGATCCAGACCATTAATCACTCTTTGGCCATTAAGTAAGTGA 718
Db 218 AAGGCTTAGATCCAGACCATTAATCACTCTTTGGCCATTAAGTAAGTGA 159
Qy 719 TTGATCTATTAAAGGATCAAGACGTCCTCCAAACCTCTCTACTATAGAGGTC 778
Db 158 TTGATCTATTAAAGGATCAAGACGTCCTCCAAACCTCTCTACTATAGAGGTC 99
Qy 779 TTATATTATAGACATCTTGTATCTGACAAAC 812
Db 98 TTATATTATAGACATCTTGTATCTGACAAAC 65
RESULT 4
AAC48359/c
ID AAC48359 standard; DNA: 754 BP.
AC AAC48359;
AT 18-OCT-2000 (first entry)
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 57192.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW Protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 990S-0121825.
PR 05-MAR-1999; 990S-0123180.
PR 09-MAR-1999; 990S-0123548.
PR 23-MAR-1999; 990S-0125788.
PR 25-MAR-1999; 990S-0126264.
PR 29-MAR-1999; 990S-0126785.
PR 01-APR-1999; 990S-0127462.
PR 06-APR-1999; 990S-0128234.
PR 08-APR-1999; 990S-0128714.
PR 16-APR-1999; 990S-0129845.
PR 19-APR-1999; 990S-0130077.
PR 21-APR-1999; 990S-0130449.
PR 23-APR-1999; 990S-0130510.
PR 28-APR-1999; 990S-0130891.
PR 30-APR-1999; 990S-0131449.
PR 30-APR-1999; 990S-0132048.
PR 04-MAY-1999; 990S-0132407.
PR 05-MAY-1999; 990S-0132484.
PR 06-MAY-1999; 990S-0132485.
PR 06-MAY-1999; 990S-0132486.
PR 06-MAY-1999; 990S-0132487.
PR 07-MAY-1999; 990S-0132863.
PR 11-MAY-1999; 990S-0134256.
PR 14-MAY-1999; 990S-0134218.
PR 14-MAY-1999; 990S-0134221.
PR 14-MAY-1999; 990S-0134370.
PR 18-MAY-1999; 990S-0134768.

PR 19-MAY-1999; 990S-0134941.
PR 20-MAY-1999; 990S-0135124.
PR 21-MAY-1999; 990S-0135353.
PR 24-MAY-1999; 990S-0135629.
PR 25-MAY-1999; 990S-0136021.
PR 27-MAY-1999; 990S-0136392.
PR 28-MAY-1999; 990S-0136782.
PR 01-JUN-1999; 990S-0137222.
PR 03-JUN-1999; 990S-0137528.
PR 04-JUN-1999; 990S-0137502.
PR 07-JUN-1999; 990S-0137724.
PR 08-JUN-1999; 990S-0138094.
PR 10-JUN-1999; 990S-0138540.
PR 14-JUN-1999; 990S-0138847.
PR 16-JUN-1999; 990S-0139119.
PR 16-JUN-1999; 990S-0139452.
PR 16-JUN-1999; 990S-0139453.
PR 17-JUN-1999; 990S-0139492.
PR 18-JUN-1999; 990S-0139454.
PR 18-JUN-1999; 990S-0139455.
PR 18-JUN-1999; 990S-0139456.
PR 18-JUN-1999; 990S-0139457.
PR 18-JUN-1999; 990S-0139458.
PR 18-JUN-1999; 990S-0139459.
PR 18-JUN-1999; 990S-0139460.
PR 18-JUN-1999; 990S-0139461.
PR 18-JUN-1999; 990S-0139462.
PR 18-JUN-1999; 990S-0139463.
PR 18-JUN-1999; 990S-0139750.
PR 18-JUN-1999; 990S-0139763.
PR 21-JUN-1999; 990S-0139817.
PR 22-JUN-1999; 990S-0139899.
PR 23-JUN-1999; 990S-0140353.
PR 23-JUN-1999; 990S-0140354.
PR 24-JUN-1999; 990S-0140695.
PR 28-JUN-1999; 990S-0140823.
PR 29-JUN-1999; 990S-0140991.
PR 30-JUN-1999; 990S-0141287.
PR 01-JUL-1999; 990S-0141842.
PR 01-JUL-1999; 990S-0142154.
PR 02-JUL-1999; 990S-0142055.
PR 06-JUL-1999; 990S-0142390.
PR 08-JUL-1999; 990S-0142803.
PR 09-JUL-1999; 990S-0142920.
PR 12-JUL-1999; 990S-0142977.
PR 13-JUL-1999; 990S-0143542.
PR 14-JUL-1999; 990S-0143624.
PR 15-JUL-1999; 990S-0144005.
PR 16-JUL-1999; 990S-0144085.
PR 16-JUL-1999; 990S-0144086.
PR 19-JUL-1999; 990S-0144331.
PR 19-JUL-1999; 990S-0144332.
PR 19-JUL-1999; 990S-0144333.
PR 19-JUL-1999; 990S-0144334.
PR 19-JUL-1999; 990S-0144335.
PR 20-JUL-1999; 990S-0144352.
PR 20-JUL-1999; 990S-0144632.
PR 20-JUL-1999; 990S-0144884.
PR 21-JUL-1999; 990S-0144814.
PR 21-JUL-1999; 990S-0145086.
PR 21-JUL-1999; 990S-0145088.
PR 22-JUL-1999; 990S-0145088.
PR 22-JUL-1999; 990S-0145087.
PR 22-JUL-1999; 990S-0145089.
PR 22-JUL-1999; 990S-0145192.
PR 23-JUL-1999; 990S-0145145.
PR 23-JUL-1999; 990S-0145218.
PR 23-JUL-1999; 990S-0145224.
PR 26-JUL-1999; 990S-0145276.
PR 27-JUL-1999; 990S-0145913.
PR 27-JUL-1999; 990S-0145918.
PR 27-JUL-1999; 990S-0145919.

PR 28-JUL-1999; 99US-0145951.
 PR 02-AUG-1999; 99US-0146386.
 PR 02-AUG-1999; 99US-0146388.
 PR 02-AUG-1999; 99US-0146389.
 PR 03-AUG-1999; 99US-0147038.
 PR 04-AUG-1999; 99US-0147204.
 PR 04-AUG-1999; 99US-0147302.
 PR 05-AUG-1999; 99US-0147192.
 PR 05-AUG-1999; 99US-0147260.
 PR 06-AUG-1999; 99US-0147303.
 PR 06-AUG-1999; 99US-0147416.
 PR 09-AUG-1999; 99US-0147493.
 PR 09-AUG-1999; 99US-0147935.
 PR 10-AUG-1999; 99US-0148171.
 PR 11-AUG-1999; 99US-0148319.
 PR 12-AUG-1999; 99US-0148341.
 PR 13-AUG-1999; 99US-0148565.
 PR 13-AUG-1999; 99US-0148684.
 PR 16-AUG-1999; 99US-0149368.
 PR 17-AUG-1999; 99US-0149175.
 PR 18-AUG-1999; 99US-0149426.
 PR 20-AUG-1999; 99US-0149722.
 PR 20-AUG-1999; 99US-0149723.
 PR 20-AUG-1999; 99US-0149929.
 PR 23-AUG-1999; 99US-0149902.
 PR 23-AUG-1999; 99US-0149930.
 PR 25-AUG-1999; 99US-0150566.
 PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151066.
 PR 27-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158025.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.
 PR 18-OCT-1999; 99US-0159584.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.

PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 80.8%; Score 692; DB 21; Length 754;
 Best Local Similarity 100.0%; Pred. No. 6,5e-152;
 Matches 692; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 TTATTACACTTATATATGAACTCTATAGGACATCACCCTGCTTACTCGATCA 180
 DB 754 TTATTACACTTATATATGAACTCTATAGGACATCACCCTGCTTACTCGATCA 695
 QY 181 TAAATGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 240
 DB 694 TAAATGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 635
 QY 241 CAATTGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 300
 DB 634 CAATTGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 575
 QY 301 TGACATTTGTAAGAACTGCGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
 DB 574 TGACATTTGTAAGAACTGCGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 515
 QY 361 CGAGTTGTAAGTTGCGGCGCCACCCTGCTGATACATGTTGCTGCGCAAGCTGCGA 420
 DB 514 CGAGTTGTAAGTTGCGGCGCCACCCTGCTGATACATGTTGCTGCGCAAGCTGCGA 455
 QY 421 AACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 480
 DB 454 AACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 395
 QY 481 ATCTCATTTGCCAAGTTGTTCCAGTTGTAGAGGAGGAGGAGGAGGAGGAGGAGG 540
 DB 394 ATCTCATTTGCCAAGTTGTTCCAGTTGTAGAGGAGGAGGAGGAGGAGGAGGAGG 335
 QY 541 TATTCGAGAGTGAAGGTTGCTAGAGCTTGGACATCTGATCCATCAATCAAGTA 600
 DB 334 TATTCGAGAGTGAAGGTTGCTAGAGCTTGGACATCTGATCCATCAATCAAGTA 275
 QY 601 TAGAAGTCTCTGAGTCTTCTCCACCAATCTCAACTCTTGCTTTGTTGAACCTGAGA 660
 DB 274 TAGAAGTCTCTGAGTCTTCTCCACCAATCTCAACTCTTGCTTTGTTGAACCTGAGA 215
 QY 661 GGCCTTAGATCCAGCATTAAGTACCTCTTTGGCCATTAAGTACCTTTAGAGTGATT 720
 DB 214 GGCCTTAGATCCAGCATTAAGTACCTCTTTGGCCATTAAGTACCTTTAGAGTGATT 155
 QY 721 GATCTATTAAAGGATCAAGAGTCTCCACCAACTCTGCTACTTAAGAGGCTCTTT 780
 DB 154 GATCTATTAAAGGATCAAGAGTCTCCACCAACTCTGCTACTTAAGAGGCTCTTT 95
 QY 781 ATATTATTAGACATCTTGTGATCTTGAACAAC 812
 DB 94 ATATTATTAGACATCTTGTGATCTTGAACAAC 63

RESULT 5
 AAA60683/C
 ID AAA60683 standard; DNA; 528 BP.
 AC AAA60683;
 XX 26-OCT-2000 (first entry)
 DT Arabidopsis thaliana nucleotide sequence seq ID NO:2.
 DE Arabidopsis thaliana; Cruciferae; plant; control; flowering;
 KW solar radiation; ds.
 XX

OS Arabidopsis thaliana.
XX JP2000139250-A.
XX
XX 23-MAY-2000.
XX
XX 11-NOV-1998; 98JP-0320219.
XX
XX 11-NOV-1998; 98JP-0320219.
XX
XX (TORA) TORAY IND INC.
XX WPI: 2000-425906/37.
XX P-PSDB: AABI2459.
XX
XX A method to accelerate plant generation and generation accelerated
XX plants -
XX
XX Claim 5; Page 5; 6pp; Japanese.
XX
CC the present invention describes a method to accelerate plant generation
CC and generation accelerated plants. The method uses a controlling gene
CC functioning in the downstream of a gene under the control of solar
CC radiation to accelerate plant generation using a gene functioning to
CC accelerate the flowering time regardless of solar radiation. The method
CC can control flowering time to a desired period by shortening the
CC juvenile stage. The present sequence represents a specifically claimed
CC Arabidopsis nucleotide sequence, which is used in the exemplification
CC of the present invention.
XX
XX
SQ Sequence 528 BP; 143 A; 111 C; 129 G; 145 T; 0 other;
Query Match 61.7%; Score 528; DB 21; Length 528;
Best Local Similarity 100.0%; Pred. No. 1.le-113;
Matches 528; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 267 CTAAGCTCTTCTCCGCGAGCAGCTCCCTCGACATTTGTAAGAAAGTGGCGCCAC 326
DB 528 CTAAGCTCTTCTCCGCGAGCAGCTCCCTCGACATTTGTAAGAAAGTGGCGCCAC 469
QY 327 GGGAGGCGGAGATGTAGATCTCAGCAAACTCCGAGTGTGAAGTTTGGCGCCACC 386
DB 468 GGGAGGCGGAGATGTAGATCTCAGCAAACTCCGAGTGTGAAGTTTGGCGCCACC 409
QY 387 TGGTCATACACTGTTCCTCCGCGAGCAGCTCCCTCGACATTTGTAAGAAAGTGGCGCCAC 446
DB 408 TGGTCATACACTGTTCCTCCGCGAGCAGCTCCCTCGACATTTGTAAGAAAGTGGCGCCAC 349
QY 447 TCCGTCAGTGGAGCTGTGATTTGCTAACACACAATCTCATTTGCCAAGGTTGTTCCAGT 506
DB 348 TCCGTCAGTGGAGCTGTGATTTGCTAACACACAATCTCATTTGCCAAGGTTGTTCCAGT 289
QY 507 TGTAGCAGGATATCAGTACCAACCAATGAGATATTTCTCGAGGTGAGGTTGCTAGG 566
DB 288 TGTAGCAGGATATCAGTACCAACCAATGAGATATTTCTCGAGGTGAGGTTGCTAGG 229
QY 567 ACTTGAACCATCTGGATTCACCATTAACCAAGTATAGAGTTCCGAGGTCTTCTCCACC 626
DB 228 ACTTGAACCATCTGGATTCACCATTAACCAAGTATAGAGTTCCGAGGTCTTCTCCACC 169
QY 627 AATCTCACTCTTGGCTGTGTTTGAAGCTGAGAAGGCTTGTAGATCCAGCCATTAGTAC 686
DB 168 AATCTCACTCTTGGCTGTGTTTGAAGCTGAGAAGGCTTGTAGATCCAGCCATTAGTAC 109
QY 687 CTCTCTTTGGCCATTAAGTACCTTTAGAGTATGATCTATTAACGATCAAGAACGTC 746
DB 108 CTCTCTTTGGCCATTAAGTACCTTTAGAGTATGATCTATTAACGATCAAGAACGTC 49
QY 747 TCCAAACAACCTGCTTACTATTAAGAGGCTCTTATATTATTAAGCAT 794
DB 48 TCCAAACAACCTGCTTACTATTAAGAGGCTCTTATATTATTAAGCAT 1

RESULT 6
AAC42966/C
ID AAC42966 standard; DNA; 528 BP.
XX
XX AAC42966;
XX
XX 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 37529.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway;
XX metabolic pathway; promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
XX 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126264.
XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0127462.
XX 06-APR-1999; 99US-0128234.
XX 08-APR-1999; 99US-0128714.
XX 16-APR-1999; 99US-0129845.
XX 19-APR-1999; 99US-0130077.
XX 21-APR-1999; 99US-0130449.
XX 23-APR-1999; 99US-0130510.
XX 28-APR-1999; 99US-0130891.
XX 30-APR-1999; 99US-0131449.
XX 30-APR-1999; 99US-0132048.
XX 04-MAY-1999; 99US-0132407.
XX 05-MAY-1999; 99US-0132484.
XX 06-MAY-1999; 99US-0132485.
XX 07-MAY-1999; 99US-0132486.
XX 07-MAY-1999; 99US-0132487.
XX 11-MAY-1999; 99US-0132863.
XX 14-MAY-1999; 99US-0134256.
XX 14-MAY-1999; 99US-0134218.
XX 14-MAY-1999; 99US-0134219.
XX 14-MAY-1999; 99US-0134370.
XX 18-MAY-1999; 99US-0134376.
XX 19-MAY-1999; 99US-0134941.
XX 20-MAY-1999; 99US-0135124.
XX 21-MAY-1999; 99US-0135353.
XX 24-MAY-1999; 99US-0135629.
XX 25-MAY-1999; 99US-0136021.
XX 27-MAY-1999; 99US-0136392.
XX 28-MAY-1999; 99US-0136782.
XX 01-JUN-1999; 99US-0137222.
XX 03-JUN-1999; 99US-0137528.
XX 04-JUN-1999; 99US-0137502.
XX 07-JUN-1999; 99US-0137724.
XX 08-JUN-1999; 99US-0138094.
XX 10-JUN-1999; 99US-0138540.
XX 10-JUN-1999; 99US-0138847.
XX 14-JUN-1999; 99US-0139119.
XX 16-JUN-1999; 99US-0139452.
XX 17-JUN-1999; 99US-0139453.
XX 17-JUN-1999; 99US-0139492.
XX 18-JUN-1999; 99US-0139454.
XX 18-JUN-1999; 99US-0139455.
XX 18-JUN-1999; 99US-0139456.
XX 18-JUN-1999; 99US-0139457.
XX 18-JUN-1999; 99US-0139458.

Qy	447	TCCTGCAGTGGGACTTGGATTTTGTGAACACCAATCTCAATTCGCCAAGGTTGTCCAGT	506
Db	348	TCCCGAGGGGGAGCTGGGACTCTGTGACACACCCTCAATTGCCAAGGCATTTTCCAGT	2899
Qy	507	TGTAGCAGGGGATATACGTACACCAACCAATGAGATATCTCGGAGGTGAGGGTTGCTAGG	566
Db	288	GGTGGCAGGTTATACGTACACCAACCGGTGAGATATCTCGTTGGTGAAGGTTGGCTTGG	2299
Qy	567	ACTTGGAAACATCTGGATGCCACCATTAACCAAGTATTAAGTCTCGTGGGCTTCTCCACC	626
Db	228	ACTGGGCACATCTGGATGCCACCATTAACCAAGTATTAAGTCTCGTGGGCTTCTCCACC	169
Qy	627	AATCTCAACTCTTGGCTTTGTTGAACTTGAGAGGCCCTTAGATCCAAAGCCATTAGTCAC	686
Db	168	AATCTCAACTTATGGTTGTTGTTGCAAACTTGAGAGGCCCTTAGATCCAAAGCCATTAGTCAC	109
Qy	687	CTCTCTTTGGCCATTAACCTTAAGTATGATCTATTAAACGATCAAGAACGTC	746
Db	108	CTCTCTATGGCCATTAAGTATGATCTATTAAACGATCAAGAACGTC	49
Qy	747	TCGCAACAACCTGCTTACTATTAAGAGGCTCTCTATATTATTAAGACAT	794
Db	48	TCGCAACAACCTGCTTACTATTAAGAGGCTCTCTATATTATTAAGACAT	1

RESULT 7
AAA60684/c
ID AAA60684 standard; DNA; 528 BP

DT 26-OCT-2000 (first entry)

DE Arabidopsis thaliana nucleotide sequence SEQ ID NO:3.

KM Arabidopsis thaliana; Cruciferae; plant; control; flowering;
KM solar radiation; ds.

05 *Arabidopsis thaliana*.

PN JP2000139250-A.

PD 23-MAY-2000.

PF 11-NOV-1998; 98JP-0320219.

PR 11-NOV-1998; 98JP-0320219.

PA (TORA) TORAY IND INC.

DR WPI; 2000-425906/37.

PT A method to accelerate plant generation and generation accelerated

XX

CC the present invention describes a method to accelerate plant generation
CC and generation accelerated plants. The method uses a controlling gene
CC functioning in the downstream of a gene under the control of solar
CC radiation to accelerate plant generation using a gene functioning to
CC accelerate the flowering time regardless of solar radiation. The method
CC can control flowering time to a desired period by shortening the
CC juvenile stage. The present sequence represents a specifically claimed
CC Arabidopsis nucleotide sequence, which is used in the exemplification
CC of the present invention.

Sequence 528 BP; 122 A; 117 C; 142 G; 147 T; 0 other;

Query Match	43.7%	Score 374.4	DB 21	Length 528
Best Local Similarity	81.8%	Pred. No. 6.9e-78		
Matches 432; Conservative	0	Mismatches 96	Indels 0	Gaps 0

QY	267	CTCAAGCTCTCTCCCTCCGACGACCTCCCTCTGACATTTGTAGAAACATCGGCCAC	326
Db	528	CTACGTTCTTTCTCCCCACAGCCATTCTCCCTCTGGCACTTAAGTAAGAGCACCCAC	469
QY	327	GGGAAGGCCGAGATTGTAGATCTTCAGCAAACTGCGCGAGTTTGAGTTCTGGCGCCACC	386
Db	468	AGGAAGACCAAGATTGTAGATCTCAGCAAACTCAGAGTGTGAACGTGTGGGCCACCC	409
QY	387	TGTGTGCTATCACTTTTGGCTGCGCAACCTGTCCAAACAATATAACGACAGATGAAT	446
Db	408	CGGTGCATAAACCGTTTGTCTTCGAGTTTCCGGAAACAATACCAACAATACGATGAAT	349
QY	447	TCTGCACTGGAGATTGGATTTTCGTACACACATCTCATTCGCAAAAGTTTTCAGT	506
Db	348	TCCCGAGGGGGAGGTGGACTCTGTGACACACACCTCATTCGCAAAAGCATTTCCAGT	289
QY	507	TGTAGCAGGATATCACTCACACCAACCAATGAGATATTTCTGCGAGGTGAGGGTTGTAAG	566
Db	288	GGTGGCAGGTATATCACTCACCAACCAAGTGAATTTCTGTTGGTGAAGGTTGTTGG	229
QY	567	ACTTGAACATCTGATGCCACCATTAACCAAGTATAGAGTTCTCGAGTCTCTCCACC	626
Db	228	ACCTGGGCATCAAGATGCCACCATTAACCAAGTGTAGAATTTCTGAAGTGTCTCTCC	169
QY	627	AATCTCAACTCTTGGCTTTGTTTAACTTGAGAAGGCTTAGATCCAGCATTTAGTCAC	686
Db	168	AATCTCACTATTGGTTGTTCACAACTTAGAAGGCTTAGATCCAGCATTTAGTAAC	109
QY	687	CTCTCTTTGGCATTAAGTACCTTTAGTAGTATGATCTATTAAACGATCAAGAACGTC	746
Db	108	CTCTCTATGGCATTAAGTAGACTTAAAGAGACCAACCTGTGAAAGATCAAGAACATC	49
QY	747	TCCAACAACCTCTGCTTACTATTAAGAGGCTCTTATATTTAATAGACAT	794
Db	48	TCCAACAACCTGCGGACCAAGAGAGATCTCTGCACTTAAGACAT	1

RESULT 8
AAC90636/c
ID AAC90636 standard; cDNA; 522 BP

AC AAC90636;

DT 20-MAR-2001 (first entry)

DE Strawberry flowering regulation protein coding sequence SEQ ID NO:
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100

KW Strawberry; flowering regulation; floral homeotic gene; field crop;

XX

XX

XX

XX

XX

PR 24-MAY-2000; 2000US-0318789.

PA (DNAP) DNA PLANT TECHNOLOGY CORP.

PI oeller P, Guttererson N;

DR WPI; 2001-025165/03.

XX

PT useful for generating

PT day-neutral flowering

PS Claim 3; Page 59-60; 97bp; English.

XX The present invention provides the nucleic acid and protein sequences of
CC a number of proteins from the strawberry which are involved in the
CC regulation of flowering. These were identified using primers based on the
CC homologous sequences from *A. thaliana*, *B. napus* and *R. sativus*. They can
CC be used in the production of transgenic field crops whose flowering is
CC regulated and the time of fruiting and harvesting can be manipulated.

XX Sequence 522 BP; 147 A; 111 C; 129 G; 135 T; 0 other;

Query Match 21.1%; Score 180.2; DB 22; Length 522;
Best Local Similarity 60.8%; Pred. No. 1.3e-32;
Matches 312; Conservative 0; Mismatches 198; Indels 3; Gaps 1;

Qy 277 CTTCTCCGCGACGACCTCCCTCGACAACTTGTAGAAAGTCCGCGACGAGGCGC 336
Db 518 CGCTCTTCTGAGACGATTCCTCTGGCATTGAGAAAGACGACGCGGAGCCG 459
Qy 337 AGATTGTAGATCTCAGCAAACTCGAGTGTGAAGTCTGGCGCACCTGTGCTATAC 396
Db 458 AACCTGTTGTCTGCAAACTTCGACTGTGGAATGTCCTTGGAAGGAGGAAATC 399
Qy 397 ACTGTTCCTGCGAAGCTGTGAAACATATTAACACGACGATGAATTCCTGCACTG 456
Db 398 ACTGTTCCTGCGAAGCTGTGAAACATATTAACACGACGATGAATTCCTGCACTG 339
Qy 457 GGACTTGATTTGCTGTAACACAACTTCGCAAGGTTGTCAGTTGTAGCAGG 516
Db 338 GGCTTCGCGAATTCATATTATTAACACCTCCCTCCAAATGTGTGTCCTCTG 279
Qy 517 ATATCAGTACCAACCAATGAGATATTCGAGGTGAGGTTGCTGAGACTTGAGACA 576
Db 278 ATGTCGCGATACCACTGCAAGTGTCTTCAGGTGAGATGACTGACGACCTGAGACA 219
Qy 577 TCTGTGATCCACATACCAAGTATAGAACTTCTGAGTCTTCTCCACCAATCTCACT 636
Db 218 TCTGTGATCCACATACCAAGTATAGAACTTCTGAGTCTTCTCCACCAATCTCACT 159
Qy 637 CTGAGCTGTTTGAACCTGAGAGGCTTGTATCCACCAAGTATGAGTCTTCTCTCT 693
Db 158 TTAGGCTGAGGTTAGAGAGGATATGATCATCCATATACCTCTCTCTCTG 99
Qy 694 TGCCATATAGTACCTTTAGAGTATGATCTATTAAGGATCAAGACCTCTCCACA 753
Db 98 GAGTGTATGATCTGATCTATTTAACTGGGTGAAACATCAATCAATCTCCAAATG 39
Qy 754 ACTGTCTACTATAGAGGCTCTTATTT 786
Db 38 ACTCTTCCACACAGAGGATCTGAGATCTTT 6

RESULT 9

AAT60140/c
ID AAT60140 standard; cDNA: 668 BP.

XX AAT60140;

DT 24-JUN-1997 (first entry)

DE Arabidopsis terminal flower1 (tfl1) cDNA.

KW Terminal flower 1; tfl1; centroradialis; cen gene; flowering;

KM transgenic plant; ss.

XX Arabidopsis thaliana var. Columbia.

XX Key Location/Qualifiers

FT CDS 16..549

FT mutation /tag- a

FT /note- b

FT /note- "tfl1-14 allele has T at position 221"

FT mutation 274
FT /tag- c
FT /note- "tfl1-13 allele has G at position 274"
FT mutation 307
FT /tag- d
FT /note- "tfl1-11 allele has G at position 307"
FT mutation 329
FT /tag- e
FT /note- "tfl1-1 allele has G at position 329"

PM W09710339-A1.

PD 20-MAR-1997.

PE 13-SEP-1996; 96W0-GB02276.

PR 13-SEP-1995; 95GB-0018731.

PA (INNE-) INNES CENT JOHN.

PI Bradley DJ, Carpenter R, Coen ES;

DR WPI: 1997-202235/18.

PS P-PSDB; AAW13945.

PT Antirrhinum majus centroradialis gene and Arabidopsis homologue,

PT tfl1 - control switching of apical meristem to floral fate, useful

PS in plant hybridisation and in control of growing season

PS Claim 12; Fig 6a; 83pp; English.

XX A cDNA clone (AAT60140) codes for the terminal flower1 (TFL1) protein
XX (AAW13945) of Arabidopsis thaliana. It was obt. from an Arabidopsis
XX expressed sequence tag clone 129D77. A genomic tfl1 clone
XX (AAT60142) has also been obt. The wild-type role of the tfl1 gene
XX is to inhibit flowering and to prevent the apical meristem from
XX switching to a floral fate. The tfl1 gene was identified as a
XX homologue of the Antirrhinum centroradialis gene (see also AAT60141).
XX The flowering characteristics of transgenic plants, esp. switching
XX of apical meristem to a floral fate and the timing of flowering,
XX can be manipulated by regulating cen or tfl1 gene expression.

SO Sequence 668 BP; 195 A; 135 C; 147 G; 191 T; 0 other;

Query Match 20.7%; Score 176.8; DB 18; Length 668;
Best Local Similarity 60.6%; Pred. No. 8.8e-32;
Matches 308; Conservative 0; Mismatches 197; Indels 3; Gaps 1;

Qy 293 TCTCCCTGTGACATTTGTAGAAAGTCCGCGACGAGGACCGGATTTAGATCTCAG 352
Db 529 TTTCTCTTTGCGCTTAAAGAGACGCGCGACAGGAGACCAAGATCATCTGACCG 470
Qy 353 CAAACTCGGAGTGTGAGTCTGCGCGCACCCGCTGCT--GCATPACCTGTTGCCGCG 409
Db 469 CAATTTAGAGTGTGAGTGTGATCTCGAAGGATTTAGGAAGATTAACACGCTCTTT 410
Qy 410 CAAGCTGTGAAACATATTAACACGACGACGATGATTTCTGCACTGGGACTTGATTT 469
Db 409 GCTTCTGCTGAAACGAAACAAACAAACATGATGATCTGATGCTGCTGGCAATTT 350
Qy 470 CGTAACACACATCTCATTTGCCAAGGTTGTCAGTTGTGACAGGATFATCAGTACCA 529
Db 349 CATAGCTCACCACTCTTTGCCAAGCATGATCTGTTGTCGCGGATGTTTGTACGA 290
Qy 530 ACCATGAGATATTCCTGCGAGGTGATGATGATGATGATGATGATGATGATGATGAT 589
Db 289 TCCAGTGAAGGTCTTTTGAAGGAGGTGATGATGATGATGATGATGATGATGATGAT 230
Qy 590 TAACCAAGTATAGAGTCTTCTGAGGTTCTCCACCAATCTCAATCTTGGCTGTTT 649
Db 229 TCACCAAGTATAGAGATCTGAGATCACACCATGATCTCAACCTTAGGCTTGAGG 170
Qy 650 GAACCTGAGAGGCTTATGATCAAGCCATTAGTACCTCTCTTGGCCATTAAGTAACT 709

KW allergenic pollen; floral meristem identity protein; gene; ss.
 XX Lolium perenne.
 XX MO200233091-A1.
 XX 25-APR-2002.
 XX 17-OCT-2001; 2001WO-AU01311.
 XX 19-OCT-2000; 2000AU-0000873.
 XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 XX (AGRE-) AGRESEARCH LTD.
 XX Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
 XX WPI; 2002-452388/48.
 XX P-PSDB; ABG60933.
 PT New substantially purified or isolated polypeptide e.g., MADS-box,
 PT CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
 PT fescue species, useful for controlling plant life cycles and/or growth
 PT phases
 XX Claim 4; Fig 30; 290pp; English.
 XX
 CC The invention describes a substantially purified or isolated polypeptide
 CC (I) from a ryegrass (Lolium sp.) or fescue (Festuca sp.) species, such as
 CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
 CC proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
 CC and HB-like proteins, or their functionally active fragments or variants.
 CC Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a
 CC vector (IV) comprising (II), is useful for modifying plant life cycles
 CC and/or growth phases, flowering processes, flowering and/or plant
 CC architecture and/or flower and/or inflorescence development in a plant,
 CC which involves introducing (II), (III) or (IV) into the plant. The
 CC individual or simultaneous enhancement or downregulation of MADS-box
 CC gene activities may alter flower, embryo and seed development, e.g.,
 CC enhance or inhibit embryo differentiation and growth or alter flower
 CC organ identity through conversion of one floral organ in another.
 CC Manipulation of CEN or HB activity in plants alters the control of phase
 CC change, flowering time and the number of leaves made before flowering.
 CC Manipulation of AP2 activity in plants alters flower organ identity
 CC through conversion of one floral organ in another, leads to a change in
 CC the number of floral organs and flowering architecture. Manipulation of
 CC flowering plant architecture has a wide range of applications such as:
 CC inducing male sterility for hybrid seed production; changing flower
 CC architecture for enhancing value of ornamentals; delaying flowering in
 CC forage grasses thus stopping the formation of less digestible stems and
 CC increasing herbage quality; altering flowering time allowing early
 CC maturing crops; delaying vegetative phase to increase biomass production;
 CC increasing branching to enhanced business in fruit trees; altering plant
 CC size e.g. shorter plant stature; and in blocking flowering and reducing
 CC release for allergenic pollen. This sequence encodes a novel floral
 CC meristem identity protein involved in floral development and a potential
 CC target for manipulating plant life cycles.
 CC
 XX Sequence 792 BP; 196 A; 181 C; 181 G; 232 T; 2 other.
 SQ
 Query Match 20.6%; Score 176; DB 24; Length 792;
 Best Local Similarity 60.0%; Pred. No. 1,4e-31;
 Matches 312; Conservative 0; Mismatches 205; Indels 3; Gaps 1;

Db 505 TGAAGGAAGGCACAGATACAGTCCCTTCCTTCTGCTGAAGACACAAAATGAAC 446
 Qy 440 GATGAATTCCTGCAGTGGGACTTGGATTTCGTAACACACATCTCATTCGCAAAAGTGG 499
 Db 445 TGTGGATTCCAATGTTGGCTTGGCTCTCATAGCTCATACCTCCGCCCAATGAAG 386
 Qy 500 TTCCAGTTGTAGCAGGATATCAGTACCAACCAATGAGATATTCGAGTGAGGAT 559
 Db 385 CATCTGTTGCCACAGTATATTAAGTACCAATCAGTGAAGATGCTCCCGCAGATACGAT 326
 Qy 560 TGTAGAGCTTGAACATCTGATTCACCATACCAAAATGATGAGTTCGAGTCTT 619
 Db 325 CACTTGGTCTGGACACATCTGGTCCGCTATACCAAAATGATGAGATGCAAGTAC 266
 Qy 620 CTCACCAATCTCAACCTTGGCTTGTGTAACCTGGAAGGCTTATGATCAACGAT 679
 Db 265 CCCCCTGAACCTTCACTCTGTTAGATACACACTGATGAGGTAGATGACCAT 206
 Qy 680 TAGTCAC--TCTCTTGGCCATAGTAACCTTGAAGTATGATTAACGAT 736
 Db 205 TGAAGACCACTTGTGTTAGTATAGTGTGCTACCATCTTACACACATGGTTAATGAT 146
 Qy 737 CAAGAAGCTTCCAAACAATCTGCTTACTATAGAGGCTC 776
 Db 145 CGAGAACTTCTCAATGACACGACCAACATATAGAGGCTC 106
 RESULT 12
 ABR82092/c
 ID ABR82092 standard; cDNA: 792 BP.
 XX
 XX ABR82092;
 XX
 DE 27-AUG-2002 (first entry)
 XX
 DE Novel floral meristem identity gene LpCENa contig #1.
 XX
 XX Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS;
 KW CEN; CEN-like protein; APETALA2; AP2; AP2-like protein; HB;
 KW Homeo-box protein; HB-like protein; plant growth; plant architecture;
 KW Inflorescence development; flower development; embryo development;
 KW seed development; flower organ identity; phase change; male sterility;
 KW hybrid seed production; herbage quality; early maturing crop;
 KW biomass increase; branching increase; blocking flowering;
 KW allergenic pollen; floral meristem identity protein; ss.
 XX
 OS Lolium perenne.
 XX
 PN MO200233091-A1.
 XX 25-APR-2002.
 PD 17-OCT-2001; 2001WO-AU01311.
 PF 19-OCT-2000; 2000AU-0000873.
 PR 19-OCT-2000; 2000AU-0000873.
 XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 XX (AGRE-) AGRESEARCH LTD.
 XX Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
 XX WPI; 2002-452388/48.
 PT New substantially purified or isolated polypeptide e.g., MADS-box,
 PT CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
 PT fescue species, useful for controlling plant life cycles and/or growth
 PT phases
 XX Claim 4; Fig 32; 290pp; English.
 XX The invention describes a substantially purified or isolated polypeptide
 CC (I) from a ryegrass (Lolium sp.) or fescue (Festuca sp.) species, such as

XX Sequence 1225 BP; 388 A; 249 C; 258 G; 330 T; 0 other;
SQ Query Match 20.6%; Score 176; DB 24; Length 1225;
Best Local Similarity 60.0%; Pred. No. 1,6e-31;
Matches 312; Conservative 0; Mismatches 205; Indels 3; Gaps 1;

QY 260 AAGCCATCTAAGTCTTCTCCCGACGACCTCCCTCGATGCAATTTAGAAAGTG 319
DB 672 AAGAACTGATTTTCAGGCGCTCCCTGGACAGCTCTCTCTGCAATTTAGAAAGTG 613
QY 320 CGGCCACGGGAGGCGGAGATTGATCTCAGCAAACTCCGAGTGTGAAGTCTGGC 379
DB 612 CAGCCACAGGAGGCGGAGATTGATCTCAGCAAACTCCGAGTGTGAAGTATATCC 553
QY 380 GCCACCCGCTGATACATCTGTTGCTCCGACGACCTCCCTCGATGCAATTTAGAAAGTG 439
DB 552 TGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 493
QY 440 GATGATTCCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 499
DB 492 TGTGATTCCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 433
QY 500 TTCAAGTGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 559
DB 432 CATCTGTTGCTCCAGGATATTTACTGACAAATCCAGTGAAGATGCTCCGAGATGAGAT 373
QY 560 TGTAGAGACTTGCAATCTGATCCAGCAATCAACCAAGTGTGAAGTGTGAGTGTG 619
DB 372 CACTGTGCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 313
QY 620 CTCACCACTCTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 679
DB 312 CCCCCTGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 253
QY 680 TAGTCAC---TCTCTTGGCCATTAAGTACCTTTAGTATGATCTATTAAACGAT 736
DB 252 TGAAGACCACTGTTGATGATTAAGTATGATGATGATGATGATGATGATGATGATGAT 193
QY 737 CAAGAACCTCTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 776
DB 192 CGAGAACCTCTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 153

RESULT 14
ABR82094/C
ID ABR82094 standard; cDNA; 787 BP.
XX
AC ABR82094;
XX
DT 27-AUG-2002 (first entry)
XX
DE Novel floral meristem identity gene *lpcena* contig #3.
XX
KW Regress: fescue; MADS-box; MADS-like protein; CENTRORADIALIS;
KW CEN-like protein; APETALA2; AP2; AP2-like protein; HB;
KW Homeo-box protein; HB-like protein; plant growth; plant architecture;
KW Inflorescence development; flower development; embryo development;
KW seed development; flower organ identity; phase change; male sterility;
KW hybrid seed production; herbage quality; early maturing crop;
KW biomass increase; branching increase; blocking flowering;
KW allergenic pollen; floral meristem identity protein; ss.
XX
OS Lolium perenne.
XX
PN WO200233091-A1.
XX
PD 25-APR-2002.
XX
PF 17-OCT-2001; 2001MO-AU01311.
XX
PR 19-OCT-2000; 2000AU-0000873.
XX

PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRESEARCH LTD.
XX Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
XX WPI: 2002-452386/48.
DR
XX
XX New substantially purified or isolated polypeptide e.g., MADS-box,
PT CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
PT fescue species, useful for controlling plant life cycles and/or growth
PT phases
XX
XX Claim 3: Fig 32; 290pp; English.
PS
XX The invention describes a substantially purified or isolated polypeptide
CC (I) from a ryegrass (Lolium sp.) or fescue (Festuca sp.) species, such as
CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
CC proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
CC and HB-like proteins, or their functionally active fragments or variants.
CC Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a
CC vector (IV) comprising (II), is useful for modifying plant life cycles
CC and/or growth phases, flowering processes, flowering and/or plant
CC architecture and/or flower and/or inflorescence development in a plant,
CC which involves introducing (II), (III) or (IV) into the plant. The
CC individual or simultaneous enhancement or downregulation of MADS-box
CC gene activities may alter flower, embryo and seed development, e.g.,
CC enhance or inhibit embryo differentiation and growth or alter flower
CC organ identity through conversion of one floral organ in another.
CC Manipulation of CEN or HB activity in plants alters the control of phase
CC change, flowering time and the number of leaves made before flowering.
CC Manipulation of AP2 activity in plants alters flower organ identity
CC through conversion of one floral organ in another. Leads to a change in
CC the number of floral organs and flowering architecture. Manipulation of
CC flowering plant architecture has a wide range of applications such as:
CC inducing male sterility for hybrid seed production; changing flower
CC architecture for enhancing value of ornamentals; delaying flowering in
CC forage grasses thus stopping the formation of less digestible stems and
CC increasing herbage quality; altering flowering time allowing early
CC maturing crops; delaying vegetative phase to increase biomass production;
CC increasing branching to enhanced business in fruit trees; altering plant
CC size e.g. shorter plant stature; and in blocking flowering and reducing
CC release for allergenic pollen. This sequence represents a contig
CC polynucleotide novel floral meristem identity protein involved in floral
CC development and a potential target for manipulating plant life cycles.
XX
SQ Sequence 787 BP; 194 A; 180 C; 179 G; 228 T; 6 other;
XX
Query Match 20.4%; Score 175; DB 24; Length 787;
Best Local Similarity 59.8%; Pred. No. 2.4e-31;
Matches 311; Conservative 0; Mismatches 206; Indels 3; Gaps 1;

QY 260 AAGCCATCTAAGTCTTCTCCCGACGACCTCCCTCGATGCAATTTAGAAAGTG 319
DB 625 AAGAACTGATTTTCAGGCGCTCCCTGGACAGCTCTCTCTGCAATTTAGAAAGTG 566
QY 320 CGGCCACGGGAGGCGGAGATTGATCTCAGCAAACTCCGAGTGTGAAGTCTGGC 379
DB 565 CAGCCACAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 506
QY 380 GCCACCCGCTGATACATCTGTTGCTCCGACGACCTCCCTCGATGCAATTTAGAAAGTG 439
DB 505 TGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 446
QY 440 GATGATTCCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 499
DB 445 TGTGATTCCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 386
QY 500 TTCAAGTGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 559
DB 385 CATCTGTTGCTCCAGGATATTTACTGACAAATCCAGTGAAGATGCTCCGAGATGAGAT 326
QY 560 TGTAGAGACTTGCAATCTGATCCAGCAATCAACCAAGTGTGAAGTGTGAGTGTG 619

Db	325	CACHTGGTCCGAGACATCTGGGTCGCCCAATACCAATGTGAATTAAGATTCGCAATGCAC	266
QY	620	CTCCACCAATCTCAACTCTTGCGCTTGTTTGAACTGAGAGAGCCCTTAGATCCAAGCCAT	679
Db	265	CCCCCTGAACCTCTACCTCTTGTTTAAATGATCACTCGTATGGGTAGACCTCATATGACAT	206
QY	680	TATGACACC---TCTCTTTGGCATAACTTAACCTTTAAGATTTGATCTTTAAAGGAT	736
Db	205	TGAAGACCAAGCTTTGTTGAGTTAATAGGTTCTACCACTTTCACACATGAGGGTTAAATGGAT	146
QY	737	CAGAAGCTCTCAACCAACTCTGTTCTACTTAAGAGGATC	776
Db	145	CGAGAACTCTCCAAATGACACGACCAACAATTAAGAGGCTC	106

/db_xref="taxon:3702"
/clone="SQ183b01F"
/clone_1id="Arabidopsis thaliana green siliques Columbia"
/tissue_type="green siliques"
/note="Vector: plusescriptli SK-; Site_1: EcorI; Site_2: XhoI"

BASE COUNT 163 a 120 c 85 g 150 t
ORIGIN

Query Match 60.3%; Score 516.4; DB 10; Length 518;
Best Local Similarity 99.8%; Pred. No. 1.9e-79;
Matches 517; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 28 TAAATATACACTTCATTTAGATAGATTAATTAATATGACACACACTATATAG 87
DB 1 TAAATATACACTTCATTTAGATAGATTAATTAATATGACACACACTATATAG 60
QY 88 TAAACACTCTCATTTTCTCCCTCTCATTTTATTATACACTTATATATGACTAC 147
DB 61 TAAACACTCTCATTTTCTCCCTCTCATTTTATTATACACTTATATATGACTAC 120
QY 148 TATAGCATATACACCTGCTGCTGCTATCATTAATGTTTAAATTAATTAAT 207
DB 121 TATAGCATATACACCTGCTGCTGCTATCATTAATGTTTAAATTAATTAAT 180
QY 208 TATAGCATATATCTCATTCAGATATGATATGATATGATATGATATGATAT 267
DB 181 TATAGCATATATCTCATTCAGATATGATATGATATGATATGATATGATAT 240
QY 268 TAAAGCTCTCTCTCCGACGACCTCTCTGACATTTGTAGAAAGTGGCCACG 327
DB 241 TAAAGCTCTCTCTCCGACGACCTCTCTGACATTTGTAGAAAGTGGCCACG 300
QY 328 GGAAGCCGAGATTTAGATCTCAGCAAACTCGGAGTGTGAAGTTGGGCCACCT 387
DB 301 GGAAGCCGAGATTTAGATCTCAGCAAACTCGGAGTGTGAAGTTGGGCCACCT 360
QY 388 GGTGCATACACTGTTTGGCTGCCAAGCTGTGAAACATATTAACACGACGATGAAT 447
DB 361 GGTGCATACACTGTTTGGCTGCCAAGCTGTGAAACATATTAACACGACGATGAAT 420
QY 448 CCTGAGTGGGACTTGGATTTTGTAAACACAACTTCATTCAGAAAGTGTTCACAT 507
DB 421 CCTGAGTGGGACTTGGATTTTGTAAACACAACTTCATTCAGAAAGTGTTCACAT 480
QY 508 GTACAGGGATATCATGACCAACCAATGAGATATTC 545
DB 481 GTACAGGGATATCATGACCAACCAATGAGATATTC 518

RESULT 2
AV562377 494 bp mRNA linear EST 07-SEP-2000
LOCUS AV562377 Arabidopsis thaliana green siliques Columbia Arabidopsis
DEFINITION thaliana cDNA clone SQ169b07F 3', mRNA sequence.
ACCESSION AV562377
VERSION AV562377.1 GI:8733803
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
JOURNAL DNA Res. 7, 175-180 (2000)
MEDLINE 20363093
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute

Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/
Location/Qualifiers
1. 494
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="SQ169b07F"
/clone_1id="Arabidopsis thaliana green siliques Columbia"
/tissue_type="green siliques"
/note="Vector: plusescriptli SK-; Site_1: EcorI; Site_2: XhoI"

BASE COUNT 155 a 113 c 81 g 145 t
ORIGIN

Query Match 57.7%; Score 494; DB 10; Length 494;
Best Local Similarity 100.0%; Pred. No. 1.4e-75;
Matches 494; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 AAATTAACACTTCATTTAGATAGATTAATTAATATGACACACACTATATAGT 88
DB 1 AAATTAACACTTCATTTAGATAGATTAATTAATATGACACACACTATATAGT 60
QY 89 AAAACACTCTCATTTTCTCCCTCTCATTTTATTATACACTTATATATGAACTACT 148
DB 61 AAAACACTCTCATTTTCTCCCTCTCATTTTATTATACACTTATATATGAACTACT 120
QY 149 ATAGCATATACACCTGCTGCTGCTATCATTAATGTTTAAATTAATTAATTAAT 208
DB 121 ATAGCATATACACCTGCTGCTGCTATCATTAATGTTTAAATTAATTAATTAAT 180
QY 209 AGATGATATATCTCATTCAGATATGATATGATATGATATGATATGATATGATAT 268
DB 181 AGATGATATATCTCATTCAGATATGATATGATATGATATGATATGATATGATAT 240
QY 269 AAAGTCTCTCTCTCCGACGACCTCTCTGACATTTGTAGAAAGTGGCCACG 328
DB 241 AAAGTCTCTCTCTCCGACGACCTCTCTGACATTTGTAGAAAGTGGCCACG 300
QY 329 GGAAGCCGAGATTTAGATCTCAGCAAACTCGGAGTGTGAAGTTGGGCCACCT 388
DB 301 GGAAGCCGAGATTTAGATCTCAGCAAACTCGGAGTGTGAAGTTGGGCCACCT 360
QY 389 GTGCATACACTGTTTGGCTGCCAAGCTGTGAAACATATTAACACGACGATGAATTC 448
DB 361 GTGCATACACTGTTTGGCTGCCAAGCTGTGAAACATATTAACACGACGATGAATTC 420
QY 449 CTGCACTGGGACTTGGATTTTGTAAACACAACTTCATTCAGAAAGTGTTCACAT 508
DB 421 CTGCACTGGGACTTGGATTTTGTAAACACAACTTCATTCAGAAAGTGTTCACAT 480
QY 509 TAGCAGGGATATCA 522
DB 481 TAGCAGGGATATCA 494

RESULT 3
AV788551 423 bp mRNA linear EST 28-MAR-2002
LOCUS AV788551 RAPL6 Arabidopsis thaliana cDNA clone RAPL06-80-B19 3',
DEFINITION mRNA sequence.
ACCESSION AV788551
VERSION AV788551.1 GI:19807341
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Atakawa,T., Shibata,K., Shingawa,A., Muramatsu,M., Hayashizaki,Y.
TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
JOURNAL DNA Res. 7, 175-180 (2000)
MEDLINE 20363093
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute

Db 250 TCTCATGCCCCCACTCACCCTGGGCTGCTGGCCGACATGAGCGGCTTGACCTGC 191
Qy 674 AGCCATAGTACCTCTCTTTGGCCATAGTAACCTTTAGATGATTTGATTAATTAACG 733
Db 190 AGCCCTTGAGACAGGCTGTTCCGGAAGGTACACCTAGGTGGTGGCCGATGAAG 131
Qy 734 GATCAAGACGCTCTCCAACTCTGCTTACTATAAGAGGCTCTCT 779
Db 130 GGTCCAGCAGCTGCCACACCCCTGCCACACGAGGCTCTCT 85

RESULT 5
B0797327 659 bp mRNA linear EST 30-JUL-2002
LOCUS B0797327
DEFINITION B0797327 Ripening Grape berries Lambda Zap II Library Vitis
vitis cdna clone RT071D11 3', mRNA sequence.
ACCESSION B0797327
VERSION B0797327.1 GI:22012293
KEYWORDS EST.
SOURCE Vitis vinifera.
ORGANISM Vitis vinifera.
REFERENCE 1 (bases 1 to 659)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Coulure, C., Dedaldecamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Romieu C.
Institut National de la Recherche Agronomique
2, place Viala, 34 060 Montpellier Cedex 01, France
Tel: 00-33-(0)4-99-61-28-62
Fax: 00-33-(0)4-99-61-28-57
Email: romieu@ensam.inra.fr
Seq primer: T7.
Location/Qualifiers
1. 659
/organism="Vitis vinifera"
/cultivar="Shiraz"
/db_xref="taxon:29760"
/clone="RT071D11"
/dev_stage="ripening stage"
/note="Organ: Fruit; Vector: Lambda Zap II; Site: 1: Eco RI
; Site: 2: XhoI; Oriented library construction described
in Generation of ESTs from grape Berry (skin, pulp or
seeds) at various developmental stages by Terrier, N.,
Ageorges, A., Abbal, P., Romieu, C. in J. Plant Physiol. 158
(12): 1575-83 2001"

BASE COUNT 197 a 155 c 124 g 183 t
ORIGIN

Query Match 27.1%; Score 231.6; DB 14; Length 659;
Best Local Similarity 74.6%; Pred. No. 1.5e-30;
Matches 291; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

Qy 268 TAAAGTCTCTCTCCGCGACGACCTGCTCCCTGACATGTAGAAACATCGCGCCAGC 327
Db 270 TATATCTTTCGACACCGAGCGCCCTCTTGGCGATTAAATAAACGACGACA 329
Qy 328 GGAAGCGGAGATTTAGATCTCAGCAAACTCGGAGTGTGAAGTCTCGCGCACCT 387
Db 330 GCGAACAAGATATAAGCTGACGAAAGTCCCTAGTGTGAATTTTGGCCGACCT 389
Qy 388 GGTGCATACACTGTTGCTCGTCGCAAGCTGTGCAATATATAACAGACGATGATT 447
Db 390 GTTCATACACTGTTGCTCGTCGTCACCAAGTGGGAAACATACAAAACAGCATGATC 449
Qy 448 CCTGACATGGGACTTGTGATTTTCTAAGACACATCTCATTTGCCAAGGTTGTTCCAGTT 507

Db 450 CCAGCTGTGGGCGCTGGGCTCTCATACACAACTCTTGCGCCAGATTTGCCACAGA 509
Qy 508 GTAGAGGATATCATGATACCAACCAATGATATTTCTCGGAGTGAGGTTGTAGGA 567
Db 510 GTTGTGGAAATATCAGTACCAACCAATGATATTTCTCGGAGTTGTAGGTTGTAGG 569
Qy 568 CTTGGAACATCTGATTCACCAATCAATGATATTTCTCGGAGTTGTAGGTTGTAGG 627
Db 570 CTTGAGCGTCAAGGCTCCACCATTAACCAAGATATGAAGTCTCTCAAGTATCCCTCCA 629
Qy 628 ATCTCACTCTTGCTTTGTAACCTGA 657
Db 630 ATGTCACCCCTTAAGTTGGCTGACTAGCTGA 659

RESULT 6
AV560420 206 bp mRNA linear EST 07-SEP-2000
LOCUS AV560420
DEFINITION AV560420 Arabidopsis thaliana green siliques Columbia Arabidopsis
thaliana cdna clone S0134d05F 3', mRNA sequence.
ACCESSION AV560420
VERSION AV560420.1 GI:8731846
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 206)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 153-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
1. 206
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="S0134d05F"
/clone_1bp="Arabidopsis thaliana green siliques Columbia"
/tissue_type="green siliques"
/note="Vector: pInscriptII SK-; Site: 1: EcoRI; Site: 2:
XhoI"

BASE COUNT 69 a 43 c 28 g 66 t
ORIGIN

Query Match 24.1%; Score 206; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 6.4e-26;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 118 TTTTATATACACTTATATATTTGACTATGAGGATCATACCCGTTGCTTACTGTA 177
Db 1 TTTTATATACACTTATATATTTGACTATGAGGATCATACCCGTTGCTTACTGTA 60
Qy 178 TCATTAATGCTTATTAATTAATTAATATAGATGATTAATCTCATAGATGACAA 237
Db 61 TCATTAATGCTTATTAATTAATTAATTAATAGATGATTAATCTCATAGATGACAA 120
Qy 238 TATCAATTTGTTATTAAGGAAGAACCATTAAGTCTTCTCTCGGACCACTCTCC 297
Db 121 TATCAATTTGTTATTAAGGAAGAACCATTAAGTCTTCTCTCGGACCACTCTCC 180
Qy 298 CTCGACATTTGTAAGAAACATCGCGC 323
Db 181 CTCGACATTTGTAAGAAACATCGCGC 206

RESULT 7	AV11549/c	1168 bp	mRNA	linear	HTC 26-MAY-2002
LOCUS	AV11549				
DEFINITION	Zea mays CL846.1 mRNA sequence.				
ACCESSION	AV11549				
VERSION	AV11549.1				
KEYWORDS	HTC.				
SOURCE	Zea mays.				
ORGANISM	Zea mays.				
REFERENCE	Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.				
AUTHORS	1 (bases 1 to 1168) Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitesitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.				
TITLE	Maize Mapping Project/Dupont Consensus Sequences for Design of Overgo Probes				
JOURNAL	Unpublished (2002)				
REFERENCE	2 (bases 1 to 1168) Coe,E.C.				
AUTHORS	Direct Submission				
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA				
FEATURES	Location/Qualifiers				
SOURCE	1..1168 /organism="Zea mays" /db_xref="MaizeDB:632948" /db_xref="taxon:4577" /clone="CL846.1" /clone_id="Maize Mapping Project/Dupont Consensus Library" /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACS in conjunction with the Maize Mapping Project"				
BASE COUNT	181 a 247 c 245 g 159 t 336 others				
ORIGIN					
Query Match	23.3%.	Score 199.4;	DB 11;	Length 1168;	
Best Local Similarity	48.4%;	Pred. No. 3.8e-25;			
Matches 302;	Conservative 0;	Mismatches 322;	Indels 0;	Gaps 0;	
OY	156 TCATCAGCGTCGCTACTCGTATCATATAAGTGTATTAAATTAATACATATAGATGCA	215			
DB	813 TCGTAATGTTGAGTAGTGGATGACGATCGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	754			
OY	216 TAAATCTCATCAGATGATGCAATATCAATGTTATTAAGAAGCAAGCATCTAAAGTCT	275			
DB	753 NNNCT	694			
OY	276 TCTTCCTCCGACGCCACTCTCCCTCTGCAATTTGTAGAAAACATGCGGCACGGGAAGGCC	335			
DB	693 CCTGNNNNNAAGACGCGCGCTCAGCTGCGAGTTGAAGNNNNNNNNNNNNNNNNNNNNNN	634			
OY	336 GAGATTTGAGATCTTCAGCAAACTGCGGAGTGTGAAGTTCTTGCGCCACCTGGTGTGATA	395			
DB	633 NNN	574			
OY	396 CACTGTTGGCTGCGCAACCTGTCGAACAATATAAAGCAGACAGATGAATTTCTCGCAGT	455			
DB	573 CACGCTCGCGCCCGCCACTGCTGGAAGCAGCAGCAGCAAGCGGTGATGCCATGAT	514			
OY	456 GGGACTTGATTTTTCGTAACACACATCTCATTTGCCAAAAGTTGTTCAGTTGTAGCAG	515			
DB	513 CGGCGAGAGGCTCTGTAAGATCACTCTTGCCCAATGCTGCCAGTAGTTCCGG	454			
OY	516 GATATCACTCAACCAACCAATGGAATATTTCGAGGTGAGAGGTTCAGACACTTGGAAC	575			
DB	453 AATATCGCTCAACGACGATGATGATCTCCCTTAAGTTGGGCTGCTGGCTCGGAGC	394			

QY	576	ATGTGATCCACCAATACCAAGTATAAGTCTGTGAGGCTCTCTCCACCAATCTCAC	635
DB	333	ATCCGGGTCACCAATACCAAGAGGGTATAAGTCTCTCATGTAGSTNNNNAGCTGCAC	334
QY	636	TCTTGTGCTTGTTTTGAACCTGGAAGGCGCTTAGATCCACGACCATAGTCACTCTCTTG	695
DB	333	CCTGGGCTGTGTGACACCAATGAGGCGTTGAGTCTGGACGCGTTGGACAGGTCCTGGC	274
QY	636	GCCATTAAGTAACTTTAGATGTGATTGATCTATTAAACGATTCAGACGCTCCACACAC	755
DB	273	CCCGTAGCTGACCCCTGAGAGTTGTGTGTCGCGACGAAGGGTCCAGACGCTGNNNNNN	214
QY	756	TCTGCTACTATAAGAGGGTCTCT	779
DB	213	NN	190
RESULT	8		
LOCUS	BE498304	505 bp	mRNA
DEFINITION	WHE0963_B10.C19S wheat pre-anthesis spike cDNA library Triticum aestivum cDNA clone WHE0963_B10.C19, mRNA sequence.		
ACCESSION	BE498304		
VERSION	BE498304.1	GI:9697017	
KEYWORDS	EST.		
SOURCE	bread wheat.		
ORGANISM	Triticum aestivum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae		
AUTHORS	Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Tong, J.C.		
TITLE	The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Olin Anderson US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: 5105595773 Fax: 5105595818 Email: oander@nrcp.usda.gov Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Stragagene SK primer.		
FEATURES	Location/Qualifiers		
SOURCE	1..505		
	/organism="Triticum aestivum"		
	/cultivar="Chinese Spring"		
	/db_xref="taxon:4565"		
	/clone="WHE0963_B10.C19"		
	/clone_lib="Wheat pre-anthesis spike cDNA library"		
	/tissue_type="Spike before anthesis"		
	/dev_stage="Adult plant"		
	/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site:1: EcoRI, Site:2: XhoI; Plants were grown in the greenhouse. Whole spike with awns trimmed, white, green and yellow anther were collected and total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give plasmid phagemids in the T7 Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."		
BASE COUNT	99 a	148 c	160 g
ORIGIN			98 t
Query Match	23.2%	Score 198.4;	DB 10; Length 505;
Best Local Similarity	67.3%;	Pred. No. 8.4e-25;	

Matches 280; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

QY 364 GTGTGAAGTTCTGGCCCACTGGTGACATACCTTTGGCTGCCAAGCTGTGAAAC 423
 |||||
 Db 504 GTGTGAAGTTCTGGCCCACTGGTGACATACCTTTGGCTGCCAAGCTGTGAAAC 445
 |||||
 QY 424 AATTAACACGACGATGATTCCTGCACTGGGACTTGGATTGTTGAACACCAATC 483
 |||||
 Db 444 AGTACGACGACGATGATTCCTGCACTGGGACTTGGATTGTTGAACACCAATC 385
 |||||
 QY 484 TCATTGCCAAAGTTGTTCCAGTTGTAGACAGGATATCACTACCAACCAATGAGATAT 543
 |||||
 Db 384 TCCGCCCCGACGACGACGATGTATCCGGGATATCTGACAAACCACTGGAGATAC 325
 |||||
 QY 544 TCTCGAGGTGAGGTTGCTAGACACTTGGAACTCTGATCCACCAATGAGATATG 603
 |||||
 Db 324 TCCCTAAGTTGGATGCTGTGACATCTGGGCTTACCACTACGACAGTGTAG 265
 |||||
 QY 604 AAGTCTGAGGCTTCTCCACCAATCTCAACTCTGGCTGTTGAACCTGAGAGGC 663
 |||||
 Db 264 AAGTCTGATCTATCTATGCTCCGACCTCAACCTGGGCTGGGACCACTGAGAGGC 205
 |||||
 QY 664 CTGATGACAGCAGCATATGACCTCTCTTGGCCATAGTAACTTTAGAGTATGAT 723
 |||||
 Db 204 TTGAGCTCGACGCGCTGGACAGGCTCTGTCCGAAAGTCAACCTGAGAGTGTGTC 145
 |||||
 QY 724 CTATTAAACGATCAAGACGCTCCCAACACTCTGCTACTATAGAGGCTCTCT 779
 |||||
 Db 144 CGGACGAGGCTTCACACGCTCCCAACACTCTGCAACCACTGAGAGGCTCTCT 89
 |||||

RESULT 9
 BF483056/c 491 bp mRNA linear EST 06-DEC-2000
 LOCUS WHE2314.C03_E06ZS Wheat pre-anthesis spike cDNA library Triticum
 DEFINITION whe2314.C03_E06, mRNA sequence.
 ACCESSION BF483056
 VERSION BF483056.1 GI:11566357
 KEYWORDS EST.
 SOURCE bread wheat.
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 1 (bases 1 to 491).
 Trillaceae; Triticum.

REFERENCE
 Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han,
 P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J.,
 Seaton, C.L., and Tong, J.C.
 The structure and function of the expressed portion of the wheat
 genomes - pre-anthesis spike cDNA library
 Unpublished (2000)
 CONTACT: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105595773
 Fax: 5105595818
 Email: oanderson@w.usda.gov
 Sequence have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20
 Seq primer: Stratagene SK primer.
 LOCATION/Qualifiers
 1..491

FEATURES
 source
 1..491
 /organism="Triticum aestivum"
 /cultivar="Chinese Spring"
 /db_xref="taxon:4565"
 /clone="WHE2314.C03_E06"
 /clone_lib="Wheat pre-anthesis spike cDNA library"
 /tissue_type="Spike before anthesis"
 /dev_stage="Adult plant"
 /lab_host="E. coli SOLR"
 /note="Vector: lambda Uni-ZAP XR, excised phagemid;
 Site_1: EcoRI; Site_2: XhoI; Plants were grown in the
 greenhouse. Whole spike with awns trimmed, white, green
 and yellow anther were collected and total RNA, and
 poly(A) RNA were prepared, a cDNA library was made, and
 the cDNA clones were in vivo excised to give plasmid
 phagemids in the T1 clone lab (Choi, Close, Fenton) at
 the University of California, Riverside. Plasmid DNA
 preparations and DNA sequencing were performed in the OD
 Anderson lab (all other authors)."

BASE COUNT 93 a 145 c 151 g 101 t 1 others
 ORIGIN
 Query Match 23.0%; Score 196.8; DB 12; Length 491;
 Best Local Similarity 67.5%; Pred. No. 1.0e-24;
 Matches 276; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 371 AGTTCTGGCCGACCTGTGATACATCTGTTGCTGCCAAGCTGTGAAACATATTA 430
 |||||
 Db 491 AGTTCTGGCCGACCTGTGATACATCTGTTGCTGCCAAGCTGTGAAACATATTA 432
 |||||
 QY 431 ACACGACGATGATTCCTGCACTGGGACTTGGATTGTTGAACACCAATCTCATTC 490
 |||||
 Db 431 GCACGAGGACGATGATTCCTGCACTGGGACTTGGATTGTTGAACACCAATCTCATTC 372
 |||||
 QY 491 CAAGGTTGTTCCAGTTGTAGCAGGATATCAGTACCAACCAATGAGATATTCGGA 550
 |||||
 Db 371 NGAGGATGACACGATGATTCCTGCACTGGGACTTGGATTGTTGAACACCAATGAGATATTCGGA 312
 |||||
 QY 551 GGTGAGGTTGCTGAGACTTGAACATCTGATCCACCAATGAGATATTCGGA 610
 |||||
 Db 311 GGTGAGGATGCTGTTGAGACTTGGAGCATCTGGTCTACACAGTGTATAGAGTTC 252
 |||||
 QY 611 TGAGGTTTCCACCAATCTCAACTCTGTTGTTGAACCAAGGCTTAGAT 670
 |||||
 Db 251 TCACTCTATGTCGCGCCCACTCAACCTGCTGCGGACCATGAGATGATGATGAT 192
 |||||
 QY 671 CCAAGCATTAGTACACTCTGTTGCGCATAGTAACTTAAAGTATGATGATTA 730
 |||||
 Db 191 CGCAGCCTTGACACGCTCTGTTCCAGAAAGAACTGAGAGTGTGCTCGGATGA 132
 |||||
 QY 731 ACGGATCAGACGCTCTCAACACTCTGTTGCTTAAAGGAGGCTCTCT 779
 |||||
 Db 131 AGGGGCTCCACACGCTCTGTTCCAGAAAGAACTGAGAGTGTGCTCGGATGA 83
 |||||

RESULT 10
 AV937451 542 bp mRNA linear EST 18-JAN-2002
 LOCUS AV937451/c
 DEFINITION heading stage top three leaves Hordeum vulgare subsp. spontaneum
 cDNA clone Bah1108 5', mRNA sequence.
 ACCESSION AV937451
 VERSION AV937451.1 GI:18233248
 KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. spontaneum.
 ORGANISM Hordeum vulgare subsp. spontaneum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 1 (bases 1 to 542)
 Trillaceae; Hordeum.

REFERENCE
 Sato, K., Saito, D. and Takeda, K.
 Barley EST sequencing project in NIG and Okayama Univ
 Unpublished (2002)
 CONTACT: Tadashi Shin-1
 Center for Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6656
 Fax: 81-559-81-6855
 Email: tshin@genes.nig.ac.jp.
 LOCATION/Qualifiers
 1..542

FEATURES
 source
 1..542
 /organism="Hordeum vulgare subsp. spontaneum"
 /strain="H602"

Db 259 GGGATGCTGACACCATCCAGTCAAGTACTCTTCTAGTATGATGGGTGATGGCTTGA 200
 Oy 574 ACATCTGATCCACCATATACCAAGTATAGAGTTCCTGAGTCTTCTCCACCAATCTCA 633
 Db 199 GCGTCTGATCCACCAATATCAGGGTGTGTAGAACTCTCATCTCATCTGCACCCAGAAATCA 140
 Oy 634 ACTCTGGCTCTGTTTGAACCTGACAGAGCCCTTATGATCCAAATGATGACCTCTCT 693
 Db 139 ACTCTGGCTCTTACTTACATTTGACAGATGCTCTTACTGACGACCTGCGCAGAGCTGACCTA 80
 Oy 694 TGGCCATTAAGTAACTTTAGAGTGTATGATCTATTAAACGATCAAGAGCTCTCCACA 753
 Db 79 TTGTTGATGAGGCTATCCTTAATGGAACGGTTGATGAATGATCAAGCAGATCTTGACATA 20
 Oy 754 AC 755
 Db 19 AC 18

RESULT 14

BJ448552/c

LOCUS BJ448552 671 bp mRNA linear EST 23-MAY-2002
 DEFINITION BJ448552 K. Sato unpublished cDNA library, cv. Akashiniriki
 vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone
 baak20f16 5', mRNA sequence.

ACCESSION BJ448552
 VERSION BJ448552.1 GI:21127178

KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. vulgare.
 ORGANISM Hordeum vulgare subsp. vulgare

REFERENCE 1 (bases 1 to 671)
 AUTHORS Sato, K., Saitoh, D. and Takeda, K.
 TITLE Barley EST sequencing project in NIG and Okayama Univ
 JOURNAL Unpublished (2002)
 COMMENT Contact: Tadasu Shin-i
 Center for Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshin@genes.nig.ac.jp.

FEATURES

source location/Qualifiers
 1..671
 /organism="Hordeum vulgare subsp. vulgare"
 /cultivar="Akashiniriki"
 /db_xref="taxon:112509"
 /clone="baak20f16"
 /clone_lib="K. Sato unpublished cDNA library, cv.
 Akashiniriki vegetative stage leaves"
 /tissue_type="leaves"
 /dev_stage="vegetative stage"
 BASE COUNT 189 a 142 c 166 g 173 t 1 others

ORIGIN
 Query Match 19.2%; Score 164; DB 13; Length 671;
 Best Local Similarity 60.5%; Pred. No. 6e-19;
 Matches 288; Conservative 0; Mismatches 185; Indels 3; Gaps 1;

Oy 270 AAGTCTTCTCCGCGACGACCTCCCTGACAAATTTGAAAACCTGGCGCACGGG 329
 Db 501 AAACCTTCTCCGCTGATCCACCTTCCCTTGACA--GTTGAAATATGAGAGCAGCCAC 445
 Oy 330 AAGCCGAGATTTAGATCTGACAACTCCGAGAGTGTGAGATTCTGGCGCACCTGG 389
 Db 444 AACGTTTAGGTGTACTGCGCGTGAAGTCTCTGACAGCTGAGATTGTTCGAGACGTCTG 385
 Oy 390 TGCATACACTGTTTGCCTGCCAAGCTGTGGAACAATATTAACAGACAGATGAATTC 449
 Db 384 TGCAAAACCTGATCCCTGCTGAGTGTGCGTAACAGACAATATACATCCGCTGATACC 325

Oy 450 TCCAGTGGGACTTGGATTTTCTGTAACACAACTCTCATTTGCCAAGGTTTCCAGTTGT 509
 Db 324 AGATCTTGTCTTGTGCTTTTCAATTAACRCAAGCTCTGCGCAAGCTGGACCGATTGT 265
 Oy 510 ACCAGGATATACGTACACCAACCAATGAGATATTTCTGGAGTGAAGGTTTCTAGACT 569
 Db 264 TCCAGGAGATGTGACACCATCCAGTCAAGTACCTCCCTATGATGGTGAATGGGT 205
 Oy 570 TGGAACTGTGATCCACCATTAACCAAGTATAGAGTTCCTGAGTCTTCTCCACCAAT 629
 Db 204 TGGACGCTCTGGATCCACCAATATCAGGCTGTGTAGAACTCTCATGCTCTCCACCGNA 145
 Oy 630 CTCACCTCTGGCTGTTTGAACCTGAGAGGCTTATGATCCAGCATTAAGTACCTC 689
 Db 144 ATCACTGCTGCTTACTTACATTTGACATGCTGCTTACTGACGACCTGCCAGAACTG 85
 Oy 690 TCTTGGCCATTAAGTAACTTTAGAGTGTATGATCTATTAAACGATCAAGAGCT 745
 Db 84 CCTATTGTTGATGCGCTATCCTTAATGGAACGGTTGATGAATGATCAAGACAT 29

RESULT 15

BJ315664/c

LOCUS BJ315664 597 bp mRNA linear EST 09-APR-2002
 DEFINITION BJ315664 Y. Ogihara unpublished cDNA library, Wh_yf Triticum
 aestivum cDNA clone whyf19117 5', mRNA sequence.

ACCESSION BJ315664
 VERSION BJ315664.1 GI:20121218

KEYWORDS EST.
 SOURCE bread wheat.
 ORGANISM Triticum aestivum

REFERENCE 1 (bases 1 to 597)
 AUTHORS Ogihara, Y. and Murai, K.
 TITLE Expressed genes in Triticum aestivum
 JOURNAL Unpublished (2002)
 COMMENT Contact: Tadasu Shin-i
 Center for Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshin@genes.nig.ac.jp.

FEATURES

source location/Qualifiers
 1..597
 /organism="Triticum aestivum"
 /cultivar="Chinese Spring"
 /db_xref="taxon:4565"
 /clone="whyf19117"
 /clone_lib="Y. Ogihara unpublished cDNA library, Wh_yf"
 /tissue_type="spikelet at early flowering"
 /dev_stage="Feekes' scale 6"
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
 Site.1: EcoRI; Site.2: XhoI; Plants were grown under
 hydroponic conditions at UC Davis, salt stressed for 12
 hours, and for 7 days, then dissected and frozen (Akhunov
 in J. Dvorak Lab). Total RNA was prepared from shoot
 tissue, equal quantities of RNA were pooled from the two
 samples, polyA was purified from the pooled RNA, a cDNA
 library was made, and the cDNA clones were in vivo
 excised to give plasmid phagemids in the T3 clone lab
 at the University of California, Riverside (Akhunov, Chin
 , Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).
 Plasmid DNA preparations and DNA sequencing were
 performed in the OD Anderson lab (all other authors)."

BASE COUNT 153 a 151 c 143 g 147 t 3 others
 ORIGIN

Query Match 18.4%; Score 157.2; DB 13; Length 597;
 Best Local Similarity 59.0%; Pred. No. 9.4e-18;
 Matches 289; Conservative 0; Mismatches 198; Indels 3; Gaps 1;

Db 361 CGAGTGTGAAGTTGGCGCCACCCTGGTGATACACTGTTTGGCTGCCAAGCTGCA 420
QY 421 AACAAATATAACACGACAGATGAATTCCTGACAGTGGAGCTTGATTTTGTAAACACA 480
Db 421 AACAAATATAACGACAGATGAATTCCTGACAGTGGAGCTTGATTTTGTAAACACA 480
QY 481 ATCTCATTTGCCAAGGTTGTTCCAGTTTGAAGAGGATATCACTACCAACAATGGAGA 540
Db 481 ATCTCATTTGCCAAGGTTGTTCCAGTTTGAAGAGGATATCACTACCAACAATGGAGA 540
QY 541 TATTCGAGAGGTGAGGTTGCTGAGACTGGAACATTCGATCCACCAATGAAGTA 600
Db 541 TATTCGAGAGGTGAGGTTGCTGAGACTGGAACATTCGATCCACCAATGAAGTA 600
QY 601 TAGAATTTCTGAGTCTTCTCCACCAATCTCACTTGGCTTGTGTTGAACCTGAGA 660
Db 601 TAGAATTTCTGAGTCTTCTCCACCAATCTCACTTGGCTTGTGTTGAACCTGAGA 660
QY 661 GGCCTTAGATCCAGCCATTTAGTCACTCTCTTGGCCATTAAGTAACCTTTAGAGTAT 720
Db 661 GGCCTTAGATCCAGCCATTTAGTCACTCTCTTGGCCATTAAGTAACCTTTAGAGTAT 720
QY 721 GATCTATTAAAGGATCAAGAAAGCTGCTCAACAACTGCTTACTATAAGAGGCTCTT 780
Db 721 GATCTATTAAAGGATCAAGAAAGCTGCTCAACAACTGCTTACTATAAGAGGCTCTT 780
QY 781 ATATTATAGACATCTTTGATCTTTGAACAACCTCGTGATTCCTGAGCCGCGGG 840
Db 781 ATATTATAGACATCTTTGATCTTTGAACAACCTCGTGATTCCTGAGCCGCGGG 840
QY 841 ATCCACTAGTTCTAGA 856
Db 841 ATCCACTAGTTCTAGA 856

RESULT 2

US-09-060-726A-1/C
; Sequence 1, Application US/09060726A
; Patent No. 6225530
; GENERAL INFORMATION:
; APPLICANT: Weigel, Detlef
; APPLICANT: Salk Institute
; TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY
; TITLE OF INVENTION: MODIFIED PLANTS HAVING MODULATED FLOWER DEVELOPMENT
; FILE REFERENCE: SALKINS.026A
; CURRENT APPLICATION NUMBER: US/09/060,726A
; CURRENT FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 855
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (63)...(590)
US-09-060-726A-1

Query Match 98.4%; Score 842.4; DB 4; Length 855;
Best Local Similarity 99.8%; Pred. No. 1.2e-213;

Matches 854: Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 CTCGAGTTTTTTTTTTTTTTTTTATAAATAAACACTTCAATTCATGATTAATA 60
Db 855 CTCGAGTTTTTTTTTTTTTTTTTATAAATAAACACTTCAATTCATGATTAATA 796
QY 61 TAATTATCGATCAGACATATATTAAGTAAGACATCTCAATTTCTCCCTCTCAATT 120
Db 795 TAATTATCGATCAGACATATATTAAGTAAGACATCTCAATTTCTCCCTCTCAATT 736
QY 121 TTAATTACACATTAATATTAAGTAAGTAAGACATCAACGCTGCTTACGATATCA 180
Db 735 TTAATTACACATTAATATTAAGTAAGTAAGACATCAACGCTGCTTACGATATCA 676

QY 181 TAAATGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
Db 675 TAAATGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 616
QY 241 CAATGTTATTAAGGAAGACATCTTAAGTCTTCTCTCCGACACATCTCCCTC 300
Db 615 C-ATTGTTATTAAGGAAGACATCTTAAGTCTTCTCTCCGACACATCTCCCTC 557
QY 301 TGACAAATTTGAGAAACTGGCGGACGAGGACCGGATTTGATTTGATTTGATTTG 360
Db 556 TGACAAATTTGAGAAACTGGCGGACGAGGACCGGATTTGATTTGATTTGATTTG 497
QY 361 CGAGTGTGAAGTTTGGCGCCACCCTGATGATCACTGTTTGGCTGCCAAGCTGCA 420
Db 496 CGAGTGTGAAGTTTGGCGCCACCCTGATGATCACTGTTTGGCTGCCAAGCTGCA 437
QY 421 AACAAATATAACGACAGATGAATTCCTGACAGTGGAGCTTGATTTTGTAAACACA 480
Db 436 AACAAATATAACGACAGATGAATTCCTGACAGTGGAGCTTGATTTTGTAAACACA 377
QY 481 ATCTCATTTGCCAAGGTTGTTCCAGTTTGAAGAGGATATCACTACCAACAATGGAGA 540
Db 376 ATCTCATTTGCCAAGGTTGTTCCAGTTTGAAGAGGATATCACTACCAACAATGGAGA 317
QY 541 TATTCGAGAGGTGAGGTTGCTAGGACTTGAACAATCTGATCCACCAATMAACCAAGA 600
Db 316 TATTCGAGAGGTGAGGTTGCTAGGACTTGAACAATCTGATCCACCAATMAACCAAGA 257
QY 601 TAGAAGTCTGAGGTTCTTCCACCAATCTCAACTCTTGGCTTGTGTTGAACCTGAGA 660
Db 256 TAGAAGTCTGAGGTTCTTCCACCAATCTCAACTCTTGGCTTGTGTTGAACCTGAGA 197
QY 661 GGCCTTAGATCCAGCCATTTAGTCACTCTCTTGGCCATTAAGTAACCTTTAGAGTAT 720
Db 196 GGCCTTAGATCCAGCCATTTAGTCACTCTCTTGGCCATTAAGTAACCTTTAGAGTAT 137
QY 721 GATCTATTAAAGGATCAAGAAAGCTGCTCAACAACTGCTTACTATAAGAGGCTCTT 780
Db 136 GATCTATTAAAGGATCAAGAAAGCTGCTCAACAACTGCTTACTATAAGAGGCTCTT 77
QY 781 ATATTATAGACATCTTTGATCTTTGAACAACCTCGTGATTCCTGAGCCGCGGG 840
Db 76 ATATTATAGACATCTTTGATCTTTGAACAACCTCGTGATTCCTGAGCCGCGGG 17
QY 841 ATCCACTAGTTCTAGA 856
Db 16 ATCCACTAGTTCTAGA 1

RESULT 3

US-07-644-372-1/C
; Sequence 1, Application US/07644372
; Patent No. 5416009
; GENERAL INFORMATION:
; APPLICANT: Lazzeri, Mario E.
; APPLICANT: Nutman, Thomas B.
; APPLICANT: Weis, Niklaus
; TITLE OF INVENTION: A DNA SEGMENT ENCODING A SPECIFIC
; TITLE OF INVENTION: IMMUNODIAGNOSTIC ANTIGEN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1615 L. Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/644,372
FILING DATE: 19910123
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)861-3000
TELEFAX: (202)822-0944
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 822 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 52..507
US-07-644-372-1

Query Match      8.4%; Score 71.8; DB 1; Length 822;
Best Local Similarity 51.3%; Pred. No. 5.8e-10;
Matches .217; Conservative 0; Mismatches 202; Indels 4; Gaps 2;

QY 294 CTCCTCTGACAAATGTAGAAAACGCGCCAGGAGGAGCCGAGATTGTAGATCTCAGC 353
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 637 CTCATGTTAGCCTGGAAGAGATTTCGGCACTGATTTCCCAAGTATGTTGTTGC 578
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 354 AACCTGGCAGTGTGAAGTCTGCGG---CCACCTGGTGATACACTGTTTGCCCTGCC 410
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 577 AAATCATTAATCTTAAATTTGCGGATTTCCGCAATGTGATCCGTACTTCC 518
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 411 AAGCTGTGAAACATATATAACAGACAGCATGATTCCTGAGTGGAGATTGATTTTC 470
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 517 AGTGTATTATTAACCAAGATATACAGATTAAGTCTGCTTTCCTTTCGTGACCTGA 458
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 471 GTAACACAAATCTCAATGTCGCAAGGTTG-TTCAGTGTAGCAGGAGATATCAGTACCA 529
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 457 TCCAAATATACATACACTGTCACACTGCTACATTTTGTCCAGAAATTTATATATCA 398
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 530 ACCAATGGAGATTTCTCGGAGGTGAGGTTGCTAGACTTGAACATCTGGATCCACCA 589
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 397 ACCAATGGGCGCACCTCTGGAATACGGGGTTTTTTCGAGATGCTGCGGATCAGTCA 338
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 590 TAACCAAGATATGAGTCTGAGGTCCTTCACCAATCTCACTGCTGCTGTTT 649
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 337 TAACGAGCTATATAGCTCCAGGTTCCGATCCATGATATTTGTGCGCTGATCT 278
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 650 GAACCTGAGAGGCTTAGATCCAGCCATTTAGTCACTCTCTTTGSCCTAGTAACT 709
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 277 TTACTGCGCTGGCGTAAAGTTCAFTGCCAGATTCAOCCGTGAGATTAATGTAATA 218
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 710 TTA 712
    |||
DB 217 TGA 215
    |||

RESULT 4
US-08-467-948A-3
Sequence 3, Application US/08467948A
Patent No. 5998164
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR2
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
```

```

CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2185 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 884..2062
US-08-467-948A-3

Query Match      5.5%; Score 47; DB 2; Length 2185;
Best Local Similarity 90.9%; Pred. No. 0.003;
Matches 50; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 802 CTGGAACAAACCTGCTGATTCCTGACAGCCCGGGGATCCAGTATGTTCTAGA 856
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 2018 CTCGAACCAACCTGCTGCAATTCCTGACAGCCCGGGGATCCAGTATGTTCTAGA 2072
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 5
US-08-467-947A-3
Sequence 3, Application US/08467947A
Patent No. 6090575
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR1
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,947A
```

RESULT 6
 US-08-485-455D-60/C
 Sequence 60, Application US/08485455D
 Patent No. 5712143
 GENERAL INFORMATION:
 APPLICANT: Griewe, Robert B.
 APPLICANT: Rushlow, Keith E.
 APPLICANT: Wu Hunter, Shirley
 APPLICANT: Frank, Glenn R.
 APPLICANT: Stiegler, Gary L.
 TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
 TITLE OF INVENTION: MOLECULES, AND USES THEREOF
 NUMBER OF SEQUENCES: 79
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sheridan Rosa P.C.
 STREET: 1700 Lincoln Street, Suite 3500
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80203
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/485,455D
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Connell, Gary J.
 REGISTRATION NUMBER: 32,020
 REFERENCE/DOCKET NUMBER: 2618-25-C1-3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 863-9700
 TELEFAX: (303) 863-0223
 INFORMATION FOR SEQ ID NO: 60:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 234 base pairs
 TYPE: nucleic acid

Query Match	5.5%;	Score 46.8;	DB 2;	Length 334;
Best Local Similarity	73.2%;	Pred. No. 0.0015;		
Matches	60;	Conservative	0;	Mismatches 22;
			Indels	0;
			Gaps	0;

APPLICANT: Gaines, Patrick J.
APPLICANT: Silver, Gary
TITLE OF INVENTION: FLEA AMINOPEPTIDASE PROTEINS AND USES THEREOF
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,616
FILING DATE: 05-AUG-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..234
US-08-906-616-60

Query Match
Best Local Similarity 73.2%; Pred. No. 0.0015;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 775 TCTCTATATTATAGACATCTTGATCTTGAAACAACCTGCGTGAATTCCTGCAGCC 834
DB 129 TATCTGTAGATGAGAGCGCTCATCAACCAACGCTGCGGATTCCTGCAGCC 70
QY 835 CGGGGATCCACTAGTCTAGA 856
DB 69 CGGGGATCCACTAGTCTAGA 48

RESULT 11
US-08-817-795-60/C
Sequence 60, Application US/08817795
Patent No. 6139840
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Frank, Glenn R.
APPLICANT: Heath, Andrew W.
APPLICANT: Yamaka, Miles Yamanaka
APPLICANT: Arfsten, Ann
APPLICANT: Dale, Beverly
APPLICANT: Stiegler, Gary
TITLE OF INVENTION: USE OF PROTEASE INHIBITORS AND
TITLE OF INVENTION: PROTEASE VACCINES TO PROTECT ANIMALS FROM FLEA
TITLE OF INVENTION: INFESTATION, AND FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES, AND USES THEREOF
NUMBER OF SEQUENCES: 119
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh

STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,795
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14442
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gary J. Connell
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..234
US-08-817-795-60

Query Match
Best Local Similarity 5.5%; Score 46.8; DB 3; Length 234;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 775 TCTCTATATTATAGACATCTTGATCTTGAAACAACCTGCGTGAATTCCTGCAGCC 834
DB 129 TATCTGTAGATGAGAGCGCTCATCAACCAACGCTGCGGATTCCTGCAGCC 70
QY 835 CGGGGATCCACTAGTCTAGA 856
DB 69 CGGGGATCCACTAGTCTAGA 48

RESULT 12
US-08-485-443B-60/C
Sequence 60, Application US/08485443B
Patent No. 6146870
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary L.
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES AND USES THEREOF
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: SHERIDAN ROSS
STREET: 1700 LINCOLN ST., SUITE 3500
CITY: DENVER
STATE: CO
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,443B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary L.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C1-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303 863-9700
TELEFAX: 303 863-0223
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..234
US-08-485-443B-60

Query Match 5.5%; Score 46.8; DB 3; Length 234;
Best Local Similarity 73.2%; Pred. No. 0.0015;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

OY 775 TCTCTAATTTATAGACATCTTGTGAAACAACCTCGTGAATTCCTGCAGCC 834
DB 129 TATCTGTAAATGAGACCGCTCAATCCAAACGCTCGGCGAATTCCTGCAGCC 70
OY 835 CGGGGATCCACTAGTTCTAGA 856
DB 69 CGGGGATCCACTAGTTCTAGA 48

RESULT 13
US-08-639-075A-60/C
Sequence 60, Application US/08639075A
Patent No. 6150125
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J.
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/639,075A
FILING DATE: 24-APR-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..234
US-08-639-075A-60

Query Match 5.5%; Score 46.8; DB 3; Length 234;
Best Local Similarity 73.2%; Pred. No. 0.0015;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

OY 775 TCTCTAATTTATAGACATCTTGTGAAACAACCTCGTGAATTCCTGCAGCC 834
DB 129 TATCTGTAAATGAGACCGCTCAATCCAAACGCTCGGCGAATTCCTGCAGCC 70
OY 835 CGGGGATCCACTAGTTCTAGA 856
DB 69 CGGGGATCCACTAGTTCTAGA 48

RESULT 14
US-09-012-431-60/C
Sequence 60, Application US/09012431
Patent No. 6180383
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J.
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,431
FILING DATE: 23-Jan-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,075
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

```

?      TOPOLOGY: linear
?      MOLECULE TYPE: cDNA
?      FEATURE:
?      NAME/KEY: CDS
?      LOCATION: 1..234
?      SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-09-012-431-60

Query Match          5.5%   Score 46.8; DB 4; Length 234;
Best Local Similarity 73.2%; Pred. No. 0.0015;
Matches 60; Conservative 0; Mismatches 22; Indels 0; Gaps 0.

QY    775 TCTCTAATATTANAGACATCTTTGATCTTGACAACAACCCTCGTGTGAATTCCTGCAGCC 834
       | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     129 TATCTTTAGATGAGAGCGCCTCAATCCAAACCAAGCGTCTGCCGAATTCCTGCAGCC 70

QY    835 CGGGGGATCCACTAGTCTAGA 856
       |||||
Db     69 CGGGGGATCCACTAGTCTAGA 48
```

```

RESULT 15
US-09-012-692-60/c
: Sequence 60, Application US/09012692
: Patent No. 6214579
: GENERAL INFORMATION:
: APPLICANT: Grieve, Robert B.
: APPLICANT: Rushlow, Keith E.
: APPLICANT: Wu Hunter, Shirley
: APPLICANT: Frank, Glenn R.
: APPLICANT: Stiegler, Gary
: APPLICANT: Gaines, Patrick J.
: APPLICANT: Silver, Gary
: TITLE OF INVENTION: RNA PROTEASE PROTEINS, NUCLEIC ACID
: TITLE OF INVENTION: MOLECULES AND USES THEREOF
: NUMBER OF SEQUENCES: 190
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sheridan Ross & McIntosh
: STREET: 1700 Lincoln Street, Suite 3500
: CITY: Denver
: STATE: Colorado
: COUNTRY: USA
: ZIP: 80203
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/012.692
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/639,075
: FILING DATE: 24-APR-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Connell, Gary J.
: REGISTRATION NUMBER: 32,020
: REFERENCE/DOCKET NUMBER: 2618-25-C2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (303) 863-9700
: TELEFAX: (303) 863-0223
: INFORMATION FOR SEQ ID NO: 60:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 234 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..234
: US-09-012-692-60

```

[illegible]

Search completed: May 1, 2003, 21:56:17
Job time : 64 secs

	Query Match	100.0%	Score 856:	DB 10;	Length 856;	
	Best Local Similarity	100.0%;	Pred. No.	9e-206;		
	Matches 856:	Conservative	100.0%;	Mismatches 0;	Indels 0;	Gaps 0;
OY	1 CTCGAGTTTCTTTTTTTTTTTTTTTTTTAATAATATAACACTTCATTGCATGTAGATTAATA	60				
Db	1 CTCGAGTTTCTTTTTTTTTTTTTTTTTTAATAATATAACACTTCATTGCATGTAGATTAATA	60				
OY	61 TAATTATCGCATCACACACTATATAGTAAACACTCCTCAATTTCCGCCCTCTCATTT	120				
Db	61 TAATTATCGCATCACACACTATATAGTAAACACTCCTCAATTTCCGCCCTCTCATTT	120				
OY	121 TTAATNACACCTAATATATGTGAACATATAGGGATCTCATACCGCTTGCTACTGTATCA	180				
Db	121 TTAATNACACCTAATATATGTGAACATATAGGGATCTCATACCGCTTGCTACTGTATCA	180				
OY	181 TAAAATGGTTAATTAATTAATAATCTATAGATGCATTAATCTCATCAGATATCAATAT	240				
Db	181 TAAAATGGTTAATTAATTAATAATCTATAGATGCATTAATCTCATCAGATATCAATAT	240				
OY	241 CAATTGGTTATPAAGAGAAGAACCCATPAAGTCTTCTCCGCCACCACTCTCCCTC	300				
Db	241 CAATTGGTTATPAAGAGAAGAACCCATPAAGTCTTCTCCGCCACCACTCTCCCTC	300				
OY	301 TGACAATGTGTAAGAAACATCGCGGCCGCGGGAAGGCCGAGATTTGTATGATCTCAGCAAACG	360				
Db	301 TGACAATGTGTAAGAAACATCGCGGCCGCGGGAAGGCCGAGATTTGTATGATCTCAGCAAACG	360				
OY	361 CGAGTGTGAAGTTCTGGCGCCACCCTGGTCATCACTGTTTGGCTCCCAAGCTGTGCA	420				
Db	361 CGAGTGTGAAGTTCTGGCGCCACCCTGGTCATCACTGTTTGGCTCCCAAGCTGTGCA	420				
OY	421 AACCAATPAAPAACACACACACATGAATTCCTGCACTGGGACCTTTTGCTTAACACACA	480				
Db	421 AACCAATPAAPAACACACACACATGAATTCCTGCACTGGGACCTTTTGCTTAACACACA	480				
OY	481 ATCTGATTTGCCAAGAGTTGTCTCCAGTTGTAGAGAGGATATAGTCACCAACCAATGGAGA	540				
Db	481 ATCTGATTTGCCAAGAGTTGTCTCCAGTTGTAGAGAGGATATAGTCACCAACCAATGGAGA	540				
OY	541 TATTTCTCGAGAGTGAGGGTTGCTAGACCTTGGAAATCTGTGATCCACCATTAACCAAGA	600				
Db	541 TATTTCTCGAGAGTGAGGGTTGCTAGACCTTGGAAATCTGTGATCCACCATTAACCAAGA	600				
OY	601 TAGAAGTTCCTGAGGTTCTTCCACCAATCTCACTCTTGCTGTGTTTGAACCTGAGAA	660				
Db	601 TAGAAGTTCCTGAGGTTCTTCCACCAATCTCACTCTTGCTGTGTTTGAACCTGAGAA	660				
OY	661 GGCCTTAGATCCAAACCATTAAGTACCTCTTTGGCCATTAAGTAACCTTAGAGTGATT	720				
Db	661 GGCCTTAGATCCAAACCATTAAGTACCTCTTTGGCCATTAAGTAACCTTAGAGTGATT	720				
OY	721 GATCTATTAAACGGATCAAGAAAGCTCTCCAAACACTCTGCTTACTATTAAGAGGGTCTCT	780				
Db	721 GATCTATTAAACGGATCAAGAAAGCTCTCCAAACACTCTGCTTACTATTAAGAGGGTCTCT	780				
OY	781 AATATTATAGACATCTTTGATCTTGAACAAACCTGCTGCTAATATTCCTGACGCCGGGGG	840				
Db	781 AATATTATAGACATCTTTGATCTTGAACAAACCTGCTGCTAATATTCCTGACGCCGGGGG	840				
OY	841 ATCCACTAGTCTTAGA 856					
Db	841 ATCCACTAGTCTTAGA 856					
RESULT 3						
US-09-845-849-1/c						
Sequence 1, Application US/09845849						
Patent No. US20020029395A1						
GENERAL INFORMATION:						
APPLICANT: THE SALK INSTITUTE FOR BIOLOGICAL STUDIES						
APPLICANT: WEIGEL, Detlef						

APPLICANT: KARDALISKY, Igor
TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY
MODIFIED PLANTS HAVING MODULATED FLOWER DEVELOPMENT
FILE REFERENCE: SALKINS.026DVI
CURRENT APPLICATION NUMBER: US/09/845,849
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 09/060,726
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 856
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-845-849-1

Query Match 100.0%; Score 856; DB 10; Length 856;
Best Local Similarity 100.0%; Pred. No. 9e-206;
Matches 856; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTCGAGTTTTTTTTTTTTTTTTTTTAAATATTAACACTTCATTCATGATTAATA 60
856 CTCGAGTTTTTTTTTTTTTTTTTTTAAATATTAACACTTCATTCATGATTAATA 797
61 TAATATCGCATCACACACTATATAAGTAACACTCTCATTTTCCCTCCCTCATTT 120
796 TAATATCGCATCACACACTATATAAGTAACACTCTCATTTTCCCTCCCTCATTT 737
121 TTATTAACACTTATATATTAAGTAACACTATAGCATCAGCGTTCGTTACTGATCA 180
736 TTATTAACACTTATATATTAAGTAACACTATAGCATCAGCGTTCGTTACTGATCA 677
181 TAAATGCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
676 TAAATGCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 617
241 CAATTTGTTTAAAGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
616 CAATTTGTTTAAAGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 557
301 TGACAAATTTAGAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
556 TGACAAATTTAGAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 497
361 CGAGTGTGAAGTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
496 CGAGTGTGAAGTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 437
421 AACAAATTAACAGCAGCATGATTCCTGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 480
436 AACAAATTAACAGCAGCATGATTCCTGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 377
481 ATCTCATTTGCGCAAGGTTGTTCCAGTTGTGAGAGGATATCAGTACCAACCAATGAGA 540
376 ATCTCATTTGCGCAAGGTTGTTCCAGTTGTGAGAGGATATCAGTACCAACCAATGAGA 317
541 TATTTCTCGAGGTTGAGGTTGCTAGACCTTGGAACTTGAGTCCACCAATGAGA 600
316 TATTTCTCGAGGTTGAGGTTGCTAGACCTTGGAACTTGAGTCCACCAATGAGA 257
601 TAGAAGTTCCTGAGGTTGCTTCCACCAATTCGAATCTGGGTTGTTTAACTGAGAA 660
256 TAGAAGTTCCTGAGGTTGCTTCCACCAATTCGAATCTGGGTTGTTTAACTGAGAA 197
661 GGCCTTAGATCCAAAGCATATGACCTCTCTTGGCCATTAAGAACCTTTAGAGTAT 720
196 GGCCTTAGATCCAAAGCATATGACCTCTCTTGGCCATTAAGAACCTTTAGAGTAT 137
721 GATCTTTAAGGATCAAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
136 GATCTTTAAGGATCAAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 77
781 ATATTTAAGGATCAAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 840

|||||
Db 76 ATATTTAAGGATCAAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 17
QY 841 ATCCACTAGTTCTAGA 856
Db 16 ATCCACTAGTTCTAGA 1

RESULT 4

US-09-845-849-3

Sequence 3, Application US/09845849

Patent No. US2002029395A1

GENERAL INFORMATION:

APPLICANT: THE SALK INSTITUTE FOR BIOLOGICAL STUDIES

APPLICANT: WEIGEL, Detlef

APPLICANT: KARDALISKY, Igor

TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY

MODIFIED PLANTS HAVING MODULATED FLOWER DEVELOPMENT

FILE REFERENCE: SALKINS.026DVI

CURRENT APPLICATION NUMBER: US/09/845,849

CURRENT FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: 09/060,726

PRIOR FILING DATE: 1998-04-15

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 856

TYPE: DNA

ORGANISM: Arabidopsis thaliana

US-09-845-849-3

Query Match

Best Local Similarity

Matches 856; Conservative

100.0%; Score 856; DB 10; Length 856;

Pred. No. 9e-206;

Mismatches 0; Indels 0; Gaps 0;

1 CTCGAGTTTTTTTTTTTTTTTTTTTAAATATTAACACTTCATTCATGATTAATA 60
1 CTCGAGTTTTTTTTTTTTTTTTTTTAAATATTAACACTTCATTCATGATTAATA 60
61 TAATATCGCATCACACACTATATAAGTAACACTCTCATTTTCCCTCCCTCATTT 120
61 TAATATCGCATCACACACTATATAAGTAACACTCTCATTTTCCCTCCCTCATTT 120
121 TTATTAACACTTATATATTAAGTAACACTATAGCATCAGCGTTCGTTACTGATCA 180
121 TTATTAACACTTATATATTAAGTAACACTATAGCATCAGCGTTCGTTACTGATCA 180
181 TAAATGCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
181 TAAATGCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 240
241 CAATTTGTTTAAAGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
241 CAATTTGTTTAAAGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
301 TGACAAATTTAGAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
301 TGACAAATTTAGAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
361 CGAGTGTGAAGTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
361 CGAGTGTGAAGTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
421 AACAAATTAACAGCAGCATGATTCCTGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 480
421 AACAAATTAACAGCAGCATGATTCCTGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 480
481 ATCTCATTTGCGCAAGGTTGTTCCAGTTGTGAGAGGATATCAGTACCAACCAATGAGA 540
481 ATCTCATTTGCGCAAGGTTGTTCCAGTTGTGAGAGGATATCAGTACCAACCAATGAGA 540
541 TATTTCTCGAGGTTGAGGTTGCTAGACCTTGGAACTTGAGTCCACCAATGAGA 600
TATTTCTCGAGGTTGAGGTTGCTAGACCTTGGAACTTGAGTCCACCAATGAGA 600

Db 541 TATTCGGAGGTGAAGGTTGCTAGACTTGGACATCTGGATTCACCAATTAACCAAGTA 600
Oy 601 TAGAAGTTCCTGAGGTTCTTCTCCACCATTCTCACTCTGCTGTTTGAACCTGAGA 660
Db 601 TAGAAGTTCCTGAGGTTCTTCTCCACCATTCTCACTCTGCTGTTTGAACCTGAGA 660
Oy 661 GGCCTTAGATCCAAACCATTAATGACCTCTCTTTGGCCATAAGTAACCTTAGAGTAT 720
Db 661 GGCCTTAGATCCAAACCATTAATGACCTCTCTTTGGCCATAAGTAACCTTAGAGTAT 720
Oy 721 GATCTATTAAACGATCAAGAGCTCTCCAAACACTCTGCTAGTATAGAGGCTCTCT 780
Db 721 GATCTATTAAACGATCAAGAGCTCTCCAAACACTCTGCTAGTATAGAGGCTCTCT 780
Oy 781 ATATTATAGACATCTTGATCTTGATCAACAAACCTGCTGTAATTCCTGACCCCGGGG 840
Db 781 ATATTATAGACATCTTGATCTTGATCAACAAACCTGCTGTAATTCCTGACCCCGGGG 840
Oy 841 ATCCACTAGTCTAGA 856
Db 841 ATCCACTAGTCTAGA 856

RESULT 5

US-09-938-842A-2635/C
Sequence 2635, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SAME, AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2635
LENGTH: 528
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-2635

Query Match 44.1%; Score 377.6; DB 9; Length 528;
Best Local Similarity 82.2%; Pred. No. 2,1e-85;
Matches 434; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

Oy 267 CTAAAGTCTTCTCTCCGCGACCTCTCCCTCTGACATTTGTGAAGAACTGCGGCCAC 326
Db 528 CTAGCTTTCTTCCCGACGACCTCTCTCCCTCTGCGAGTGAAGAGCGGCCAC 469
Oy 327 GGAAGCGCCGATGTAGATCTCAGCAACTCGCGAGTGTGAAGTGTGCGGCCACCC 386
Db 468 AGGAAGACCAAGATGTGATCTCAGCAACTCAGCAAGTGTGAAGTGTGCGGCCACCC 409
Oy 387 TGTGTGATACACTGTTGCTGCGCAAGCTGTGAAACAATATAACAGACAGATGAT 446
Db 408 CGGTGATTAACCGTTTCTTCCGAGTTGCGGAAACAATACACACAAATAGATGAT 349
Oy 447 TCCGTGATGGGACTTGTGATTTGTGTAACACACAATCTCATTTGCCAAAGTTTCCAGT 506
Db 348 TCCGAGGGGGAGCGTGTGATCTGTAGCACACACCTCATTTGCCAAAGGATTTCCAGT 289
Oy 507 TGTAGAGGATATCAGTCAACCAACCAATGAGATATTCTCGAGGAGTGGGTTGCTAG 566
Db 288 GTGTGAGGATATCAGTCAACCAACCAAGTGAATATTCTGTGTGGGTTGCTTGG 229

Oy 567 ACTTGACATCTGATTCACCATTAACCAAGTATAGAGTTCCTGAGTCTTCTCCACC 626
Db 228 ACTGCGACATCTGATTCACCATTAACCAAGTATAGAGTTCCTGAGTCTTCTCCACC 169
Oy 627 AATCTCACTCTGCTGTTTGTGAACCTGAGAGGCTTGTAGATCCAAACCTTAGTAC 686
Db 168 AATCTCACTATTTGTTGTTTGTGAGAGCTGAGAGGCTTGTAGATCCAAACCTTAGTAC 109
Oy 687 CTCTCTTGGCCATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 746
Db 108 CTCTCTATGCGCATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 49
Oy 747 TCCAAACAACTCTGCTTACTATTAAGAGGCTCTCTTATTTATTAAGACAT 794
Db 48 TCCAAACAACTCTGCGACACCAAGAGATCTCTAGACTTAAGACAT 1

RESULT 6

US-09-938-842A-1501/C
Sequence 1501, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SAME, AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1501
LENGTH: 534
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-1501

Query Match 20.7%; Score 176.8; DB 9; Length 534;
Best Local Similarity 60.6%; Pred. No. 7,8e-35;
Matches 308; Conservative 0; Mismatches 197; Indels 3; Gaps 1;

Oy 293 TCTCCCTGACATTTGAGAAAGCTGCGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 352
Db 514 TTTCTCTTGTGCGTTAAAGAGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 455
Oy 353 CAACCTCCGAGTGTGAAGTCTGCGCCAGCCCGT---GATACACTGTTGCTGCG 409
Db 454 CAATTTACAGGTGTGAAGTATCTGCAAGGAGATTTAGGAAGGATTAACACGCTTTT 395
Oy 410 CAAGCTGTGAAACAATATAACAGACAGATGATGATGATGATGATGATGATGATGATGAT 469
Db 394 GCTTGTGCTGACAGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 335
Oy 470 CGTAACACAACTCATTTGCAAGGTTGTTCCAGTTGTAGCAGGAGTATCAGTACCA 529
Db 334 CATAGCTACACACCTCTTGTGCAAAAGTATGATGATGATGATGATGATGATGATGATGAT 275
Oy 530 ACCAATGAGATTTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 589
Db 274 TCCAGTCAAGGTTCTTTAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 215
Oy 590 TAACCAAGTATAGAGTTCCTGAGGCTTCTCCCAACCAATCTCAACCTTGGCTTGT 649
Db 214 TCACCAAGTATAGAGGATCTGAGATCAACCAACCAATGATCTCAACCTTGGCTTGGAG 155

QY 787 ATAGACATCTTTGATCTTGACAAACCTCTGCTGTAATTCCTGCAGCCCCGGGGGATCCAC 846

Db 145 AAAACCCCTAAATTAATTAATTAATCTGCGCAATTCCTGACGCCGGGATCCAC 86
QY 847 TACTCTAGA 856
|||||
Db 85 TACTCTAGA 76

RESULT 10
US-10-074-095-248
Sequence 248, Application US/10074095
Publication No. US2003007704A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC008C1
CURRENT APPLICATION NUMBER: US/10/074,095
CURRENT FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: 09/764,860
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/218,290
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/225,757
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/226,868
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/216,647
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/225,267
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/216,880
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/225,270
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/251,869
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/235,834
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/234,274
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: 60/234,223
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: 60/228,924
PRIOR FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/224,518
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/236,369
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/224,519
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,964
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/241,809
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/249,299
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/236,327
PRIOR FILING DATE: 2000-09-29

PRIOR APPLICATION NUMBER: 60/241,785
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/244,617
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/225,268
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/236,368
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/251,856
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/251,868
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/229,344
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/234,997
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: 60/229,343
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229,345
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229,287
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229,513
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/231,413
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/229,509
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/236,367
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/237,039
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/237,038
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/236,370
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/236,802
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/237,037
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/237,040
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/240,960
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/239,935
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/239,937
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/241,787
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/246,474
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/246,532
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/249,216
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,210
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/226,681
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/225,759
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/225,213
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/227,182
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/225,214
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/235,836
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/230,438
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/215,135

	Query Match	5.6%	Score 48.2	DB 9	Length 367
	Best Local Similarity	76.6%	Pred. NO. 0.016		
	Matches 59	Conservative	0	Mismatches 18	Indels 0
					Gaps 0
QY	780	TATATTATAGACATCTTGATCTTGACAAACCTCGCTCTAATTCCTGCACCGCGGG	839		
DB	229	TGTGTCCTAAAGATATGTCGTCTAGTTTCTCGCGACCAATTCCTGCACCGCGGG	288		
QY	840	GATCCACTAGTCTTCTAGA	856		

Query Match	5.6%	Score 48.2;	DB 10;	Length 367;	--
Best Local Similarity	76.6%;	Pred. No. 0.016;			
Matches 59; Conservative	0;	Mismatches 18;	Indels 0;	Gaps 0;	

Db 289 GATCCACTAGTCTAGA 305

```
Query Match      5.68; Score 48; DB 10; Length 551;
Best Local Similarity 75.08; Pred. No. 0.022;
Matches 60; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
```

QY	777	TCTATATTATTAGACACTCTTGTCTTTGGACAACACCTCGGGTGATTCCTGGAGCCG	836
Db	145	TCCCAAGCTTATACGCTGACGCCCTCTGTGATGGCTGCTGCTGCGGATTCCTCGACGCCG	86
QY	837	GGGATGCACCTAGTTCTAGA	856
Db	85	GGGATCCACCTAGTTCTAGA	66

RESULT 13

```

US-09-764-868-303/c
: Sequence 303, Application US/09764868
: Patient No. US20020168711A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PT232
: CURRENT APPLICATION NUMBER: US/09/764,868
: CURRENT FILING DATE: 2001-01-17
: Prior application data removed - refer to PALM or file wrapper
: NUMBER OF SEQ ID NOS: 1510
:
: SOFTWARE: PatentIn Ver. 2.0
:
: SEQ ID NO 303
:
: LENGTH: 2585
:
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
: US-09-764-868-303

```

Query Match	5.68;	Score 47.8;	DB 9;	Length 2585;
Best Local Similarity	96.18;	Pred. NO. 0.054;		
Matches 49;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

Oy 806 AACAAACCTCGTGCCTGAATTCCGTGACCCCCGGGGATCCACTAGTTCTAGA 856
|| |||||
Db 60 AAAAACCTCGTGCGAATTCCGTGACCCCGGGGATCCACTAGTTCTAGA 10

RESULT 14

```

US-09-925-297-400/c
Sequence 400, Application US/09925297
Patent No. US20020081659A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 400
LENGTH: 560
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (7)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (10)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (14)
OTHER INFORMATION: n equals a,t,g, or c
US-09-925-297-400

```

Query Match	5.68;	Score 47.6;	DB 10;	Length 560;
Best Local Similarity	75.68;	Pred. No. 0.028;		
Matches	59;	Conservative	0;	Mismatches 19;
				Indels 0

[illegible]

RESULT 15

```

US-09-764-891-404/c
; Sequence 404, Application US/09764891
; Publication No. US20030077808a1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764, 891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 404

```

```

: LENGTH: 631
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (19)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: SITE
: LOCATION: (27)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: SITE
: LOCATION: (28)
: OTHER INFORMATION: n equals a,t,g, or c
: SS-09-764-891-404

```

Query Match	5.68;	Score 47.6;	DB 9;	Length 631;
Best Local Similarity	85.58;	Pred. No. 0.029;		
Matches 53; Conservative	0;	Mismatches 9;	Indels 0;	Gaps 0;

Oy 795 CTTTGATCTTGAACAAACCCTGTCGTCAATTCCGCAGCCCGGGGGATCACAAGTTCCTA 854
 ||| | || | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 127 CTATAACGCGATCACACTCCCTGTCGCCAATTCCGCAGCCCGGGGGATCACAAGTTCCTA 68

QY	855	GA	851
		11	
Db	67	GA	66

```
Search completed: May 1, 2003, 23:35:13
Job time : .159.5 secs
```